Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Q81dv1 arabidopsis
Q9fnk3 arabidopsis
Q7ull2 rhodopirell
Q9fgi1 arabidopsis
Q98214 molluscum c
Q86gj9 dictyostell
Q9cxf5 mus musculu
Q8c0b3 mus musculu
Q8c857.jembrana di
Q8t887.jembrana di
Q8t887.jembrana di
Q8t683 agrocybe ae
Q30734 macaca neme
Q30747 macaca neme
Q91213 pseudomonas
Q94ct7 oryza sativ
Q9u7p5 eufolliculi
Q9vca3 drosophila
Q9vca3 drosophila
Q9vca3 drosophila
Q9vca3 drosophila
Q9vca1 cryptospori
O57161 spinach lat
Q9vml1 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogzwij cucurbita m
Q8xfl2 salmonella
Q8z0g3 anabaena sp
Q9vwf6 drosophila
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01-07AN-1998 (TrEMBLrel. 05, Last sequence update)
01-07AN-1998 (TrEMBLrel. 25, Last annotation update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
10-10CT-2003 (TrEMBLrel 25, Last 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016620; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN III.
InterPro; IPR003957; FN III.
InterPro; IPR003528; Hemtopoptn_L_F1.
Ffam; PF00041; fan; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=98296111; PubMed=9630610;

Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,

Miyatake K., Nakano Y.;

"The intron 5-inserted form of rat erythropoietin receptor is

expressed as a membrane-bound form.";

Biochim. Biophys. Acta 1403:169-178(1998).

EMBL: D83509; BAA22373.1;

HSSP: P19235; 1EBA.
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Q8XFL2
Q8Z0G3
Q9VWF6
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                                                   07UL12
09EG11
09EG11
09EG79
09CXF5
08CXF5
08CXF3
08CXF3
08TX82
08TX82
08TX82
08TX82
08TX83
091CX3
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     Receptor; Signal
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Q28206 bos taurus.
Q27950 bos indicus
Q95n13 ovis aries
Q95n14 ovis aries
Q8tyf5 methanopyru
Q9ug52 homo sapien
Q9axx8 legionella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       035545 rattus norv
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Q91py7 arabidopsis
                                                                                                                                                                                              (without alignments)
186.075 Million cell updates/sec
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                                                                                                                                                                  May 6, 2004, 12:41:36 ; Search time 39 Seconds
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Maximum Match 100*
Listing first 45 summaries
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Q9JMB8
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_unclassified:*
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sp_bacteriap:*
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sp_bacteria:*
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Maximum DB seq length: 200000000
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sp_virus:*
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88.9
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091632 cherry gree

Length 316,

Score 109; DB 11; Pred. No. 6.8e-10;

93.2%;

Query Match Best Local Similarity

oryza sativ oryza sativ arabidopsis

Q8c6x1 Q941s6 Q7xdn4 091py7 09jmb8

094LS6 07XDN4 09ASX3

ОВС6Х1

Result Š. 29asx3

mus musculu mus musculu

POTENTIAL. POTENTIAL. ; 05C44BF8516C180B CRC64;

316 PO' 34220 MW;

316 AA;

SEQUENCE

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EMBL; U61399; AAB03871.1; -.
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229 AA;
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Q27950
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GO:0004896; F:hematopolatin/interferon-class (D200-domain. . .; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Christenson R.K., Vallet J.L.;
"Porcine Erythropoietin Receptor: Molecular Cloning and Expression in Embryonic and Fetal Liver.";
Domest. Anim. Endocrinol. 0:0-0(2000).
EMBL; AP274305; ARF77065.1;
HSSP; P19235; 1ERN.
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovimae Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Brythropoietin receptor.
Sus scrofa (Pig)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
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91.5%; Score 107; DB 6; Length 509;
Best Local Similarity 91.3%; Pred. No. 2.5e-09;
Matches 21; Conservative 1; Mismatches 1; Indels
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           1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Erythropoietin receptor (Fragment).
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PROSITE; PS00559; MOLYBDOPTERIN EUK; 1.
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Interpro; IRR003961; FN III.
Interpro; IPR008957; FN III-like.
Interpro; IPR008528; Hemtopoptn L-F1.
Interpro; IPR00572; Oxidored_molyb.
Pfam; PF00041; FN3; 1.
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               21; Conservative
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Skaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004895; P:hematopoietim/interferon-class (D200-domain.
GO; GO:0004872; P:receptor activity; IEA.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_F1.
Pfam; PF00041; fn3; 1.
SWART; SM00060; FN3; 1.
PROSITE; PS01352; HEWATOPO_REC_L_F1; 1.
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GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002996; CRIP.
InterPro; IPR003961; FN III.
InterPro; IPR008957; FN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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TISSUB-Bone marrow;
Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
Submitred (JUV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U61398; AAB03870.1; -.
HSSP; P19215; 1EBA.
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88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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229 229
229 AA; 25170 MW; EDFAA6F110D992E8 CRC64;
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25196 MW; F6E01C4AB07893E8 CRC64;
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Last annotation update)
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Ppfan; PF00041; ff3; 1.
SWART; SW00060; FN3; 1.
PROSITE; PS01352; HEWATOPO_REC_L_F1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 ORVEILDGRIECLLSNLRGGTRY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
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01-OCT-2003 (TrEMBLrel. 25, Last a
Brythropoietin receptor (Fragment)
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Methanopyrus kandleri.
Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-98146168; PubMed=9486763;
Kamei Y., Tsutsumi O., Taketani Y., Watanabe K.;
"DDM cloning and obromosomal localization of neural adhesion
                                                       Length 418;
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  418 AA; 45282 MW; BB742BBEA034503C CRC64;
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Last annotation update)
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Last annotation update)
                                                 Query Match 88.9%; Score 104; DB 6; Best Local Similarity 87.0%; Pred. No. 6.4e-09; Matches 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                       176 AA.
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47.9%; Score 56;

Best Local Similarity 52.4%; Pred. No. (
Matches 11; Conservative 4; Mismatc)
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                                                                                                                                                                                       HSSP; P20241; ICFB.
Genew; HGNC:2176; CNTN6.
GO; GO:0007155; P:cell adhesion; TAS
                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                       1 ORVEILEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 RVEILEGRIECVLSNLRGRIR 22
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uncharacterized protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. SEQUENCE 176 AA;
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     SEQUENCE
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Q9UQ52
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David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.,

David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.,

Quantitation of the mRNA levels of Epo and EpoR in various tissues in

the ovine fetus.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY029231; AAK38170.1;

EMBL, AY029231; AAK38170.1;

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004895; F:hematopoietin/interferon-class (D200-domain. .; IEA.

GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                           David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;

David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;

Vountitation of the mRNA levels of Epo and EpoR in various tissues in the ovine fetus.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AVC2932; AAK38737.1;

GO, GO:0004895; E.mematopoie:in/interferon-class (D200-domain. .; IEA.

GO, GO:0004872; F:receptor activity; IEA.

InterPro; IPR008957; FN_III.

InterPro; IPR008957; FW_III-like.

InterPro; IPR008957; FW_III-like.

InterPro; IPR0081588; Hemtopoptn_L.FI.
                                                                                                                   Brythropoietin receptor (Fragment).

Vois aries (Sheep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

Bovidae, Caprinae, Ovis.
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Ovis aries (Sheep).

Bukaryota, Metazoa; Chordata; Craniata, Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.
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87.0%; Pred. No. 5.9e-09;
tive 2; Mismatches 1; Indels
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                                                                         Last sequence update)
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Last annotation update)
  387 AA
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PROSITE; PS01352; HEMATOPO_REC_L_P1; 1.
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SMART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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InterPro; IPR008957; FW_III-like.
InterPro; IPR003528; Hemtopoptn_L_FI.
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                                                 Created)
  PRT;
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                                            01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19,
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PRELIMINARY;
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                                                                                                   01-OCT-2003 (TrEMBLrel.
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Q95N14

RESULT 6
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STRAIN=Wistar; TISSUE=Brain; MEDLINE=97101230; PubMed=8945756;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Legionellaceae; Legionella.
NCBI_TaxID=446;
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41.9%; Score 49; DB 2; Length 826;
Best Local Similarity 42.9%; Pred. No. 25;
Matches 9; Conservative 6; Mismatches 6; Indels
            P:central nervous system development; TAS.
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SEQUENCE 826 AA, 91581 MW; 4BD5404C2665CFEF CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1. Application protein.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NB-3.
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GO, GO:0007417; P:central nervous system of InterPro; IPR003439; ABC transporter.
InterPro; IPR003461; FN_III.
InterPro; IPR003961; FN_III.like.
InterPro; IPR003598; FN_III.like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
PEam; PF00041; fn3; 4.
SWART; SW00060; FN3; 3.
SWART; SW00060; FN3; 3.
SWART; SW00060; FN3; 3.
SWART; SR0011; ABC TRANSPORTER_1; 1.
PROSITE; PS08031; IG_IKE; 6.
Immunoglobulin domain.
SEQUENCE 1028 AA; 113956 MW; 8B5AZEDZF
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Matches 10; Conservative
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P97528;
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DT 01-MAD DT 00-MAD DT 00-MAD DT 00-MAD DT 00-MAD DT 00-MAD DT 00-MAD DT 01-MAD D
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REBLY D8748; BAA13320.1; -
REBLY D8748; BAA13320.1; -
REBLY D8748; BAA13320.1; -
REBLY D87048; BAA13320.1; -
REBLY D8704009; C:membrane; IEA.
REBLY D8704009; F:ATT-binding; IEA.
REPTO; ROWGO0810; F:ATT-binding cassette. (ABC) transporter acti. .; IEA.
REPTO; RR003439; ABC transporter.
REPTO; IPR003439; ABC transporter.
REPTO; IPR003957; FW III-like.
REPTO; IPR003597; FW III-like.
REPTO; RR005598; Ig-22.
REAM; PF00041; fig. 6.
REAM; SM00408; IG-22; S.
REAM; SM00408; IG-22; S.
REAMSPORTE; PS0021; ABC TRANSPORTER_1; 1.
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Shinn P., Brooks S., Buehler B., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi B., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Lid, J., Liu A., Liu K., Liu S., Muthersky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
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"Genomic sequence for Arabidopsis thaliana BAC 123J18 from chromosome
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Ogawa J., Kaneko H., Masuda T., Nagata S., Hosoya H., Watanabe K.; "Novel neural adhesion molecules in the Contactin/F3 subgroup of the immunoglobulin superfamily: Isolation and characterization of CDNAs from rat brain."; Neurosci. Lett. 218:173-176 (1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 41.0%; Score 48; DB 10; Length 428; Local Similarity 45.5%; Pred. No. 18; Anishity 45.5%; Pred. No. 18; Indels nos 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1028 AA; 114065 MW; 47EFD8A370CF4923 CRC64;
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EMBL; AC011661; AAF16632.1; -.
SEQUENCE 428 AA; 48982 MM; 603F3FF2725622F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match
Local Similarity 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 EGFYECVAGNIRGR 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain.
SEQUENCE 1028 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
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SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
Buener M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T.,
Riggs F., Helao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
Utterback T.R., Feldblyum T.V., Quackenbush J., Salzberg S.L.,
White O., Fraser C.M.;
"Oryza sativa chromosome 10 BAC OSJNBb0011A08 genomic sequence.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
         "Analysis of the mouse transcriptome based on functional annotation
                                                                                 R MGD; MGI:1858223; Catton.

R GO; GO:0016020; C:membrane; IEA.

GO; GO:0005624; F:ATP binding; IEA.

GO; GO:0006009; F:ATP binding; IEA.

R GO; GO:0006810; P:ATP-binding cassette (ABC) transporter acti...;

R InterPro; IPR003439; ABC transporter.

R InterPro; IPR003491; FN III.

R InterPro; IPR003991; G.

R InterPro; IPR003999; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003598; IG.

R InterPro; IPR003606; IG.

R InterPro; IPR003606; IG.

R InterPro; IPR003606; IG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
0ryza sativa (Rice).
0ryza sativa (Rice).
Spermatophyta, Viridiplantee; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, Lillopsida; Poales; Poaceae;
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40.2%; Score 47; DB 10; Length 539;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B233ED300881B101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al protein.
539 AA; 60201 MW; 8EBED40239310BC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB ]
Fred. No. 47;
i, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      539 AA
                                                                                                                                                                                                                                                                                                                                                   Pfam, PP00041; fn3; 4.
Pfam; PP00047; ig; 6.
SWART; SW00660; Fn3; 4.
SWART; SW00609; IG; 6.
SWART; SW00409; IG 5.
SWART; SW00409; IG 5.
PROSITE; PS00231; ABC TRANSPORTER_1; 1.
PROSITE; PS00230; IG_KRE; 6.
PROSITE; PS00230; IG_MHC; 1.
SEQUENCE 1028 AA; 113761 MW; B233BD30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                           60,770 full-length cDNAB.";
Nature 420:563-573(2002).
EMBL; AK052972; BAC35227.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           duery match
Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
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                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti.
GO; GO:0006810; P:transport; IEA.
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SEQUENCE FROM N.A.
STRAIN=C5/7BL/6J; TISSUE=Head;
MEDLINE=223546683; PubMed=12466851;
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 11; Length 1028;
Pred. No. 47;
1; Mismatches 4; Indels (
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                                                                                          Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                           PRT; 1028 AA
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SMART; SM00408; IGG2; 5.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS00299; IG_MRG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00343; ABC transporter.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003598; IG-22.
InterPro; IPR003598; IG-22.
Pfam; PP00041; fn3; 4.
                                                                   Created)
                                                             01-OCT-2000 (TrEMBLrel. 15, Creat 01-OCT-2000 (TrEMBLrel. 15, Last 01-OCT-2003 (TrEMBLrel. 25, Last Neural recognition molecule NB-3. CNTN6 OR MNB-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 64.3%;
Matches 9; Conservative
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                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain.
SEQUENCE 1028 AA; 1
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                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
The Rice Chromosome 10 Sequencing Consortium;
In-depth view of structure, activity, and evolution of rice chromosome 10.";
Science 300:1566-1569(2003).
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Best Local Similarity 56.2%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE011102, AAP54107.1;
Hypothetical protein.
SEQUENCE 539 AA; 60201 MW; BEBED40239310BC2 CRC64;
                                         539 AA.
                                                  PRT;
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Q7XDN4
ID Q7XDN4;
DT Q7XDN4;
DT 01-OCT-:
DE HYPOTHE
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Search completed: May 6, 2004, 12:46:18 Job time : 40 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 6, 2004, 12:40:41; Search time 11 Seconds (without alignments) 108.874 Million cell updates/sec

US-10-612-885A-1 117 1 ORVEILEGRIECVLSNLRGRIRY 23 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum.DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Swimmer 42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P19235 homo sapien	_	Q07303 rattus norv	Q8g6j4 bifidobacte	Q99n43 mus musculu	_	_	Q8nq38 corynebacte	P49746 homo sapien	_		_	_	Q9urt4 schizosacch	P34434 caenorhabdi	P46942 nicotiana B		-	Q92484 rattus norv	•	corynek		-			P13663 saccharomyc	Q8z8x1 salmonella		P80096 panulirus i	_	Q63198 rattus norv	-	Q80901 human papil
SUMMARIES	ΩI		EPOR_MOUSE	EPOR_RAT	GIDB BIFLO	KRM1 MOUSE	KRM1 HUMAN	PYRB COREF	PYRB_CORGL	TSP3_HUMAN	YSS9_ENTFA	RS28_KLULA	RS28 KLUMA		AMS2 SCHPO	YL54 CAEEL	DB10 NICSY	YR33 MYCTU	AXO1 CHICK	KRM1 RAT	FPG VIBPA	MURC CORGL	TSP3 MOUSE	YA29_TREPA	PTPD_HUMAN	RS28 YEAST	DHAS_YEAST	THII SALTI	THII SALTY	HCYC PANIN	CONT_MOUSE	CONT_RAT		VE7_HPV37
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	Score	117	109	109	49	49	49	48	48	47	46	46	46	. 46	46	46	45.5	45	45	44	43.5	43	43	42.5	•	42	42	42	42	42	42	4	41.5	41
	Result No.	1	8	m	4	'n.	9	7	89	6	10	11	12	13	14	15	16	11	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33

Q97b95 thermoplasm P77161 escherichia Q60041 thermotoga Q60041 thermotoga Q9a2x6 caulobacter Q29265 archaeoglob P38867 escharcomyc P23760 homo sapien P24510 mus musculu P23759 homo sapien P11141 caenorhabdi Q52225 thermus fill P32670 escherichia
RS4_THEVO GLXR_ECOLI XYNB_THENE PROA_CAUCR YS97_ARCFU YHX7_YEAST PAX3_HUMAN PAX3_HUMAN PAX3_HUMAN HS7P_CAEEL DPOI_THEFI
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ALIGNMENTS

. (POTENTIAL).

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_L_FI.
Pfam; PF00041; fn3; 1.
PIRSF; PIRSF001959; BO_receptor; 1.
SWART; SW00060; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_FI; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 117; DB 1; Length 508; larity 100.0%; Pred. No. 8.3e-11; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                             ERYTHROPOIETIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PIERONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55065 MW; F9F326E162E9512A CRC64;
                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPOR MOUSE STANDARD; PRT; 507 AA. P1475; 91475; 91485; 163852; 14, Created) 01-ARR-1990 (Rel. 14, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Erythropoletin receptor precursor (EPO-R).
                                                                                                                                                                                                                                                                                   APS-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 QRVEILEGRTECVLSNLRGRTRY 216
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Matches 23; Conserv
                                                                                                                                                     D-structure.
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SEQUENCE
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MOD RES
CARBOHYD
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                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Crystallographic evidence for preformed dimers of erythropoietin "Crystallographic evidence for preformed dimers of erythropoietin sceptor before 11gand activation."; Science 283:987-990(1999).
-!- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-induced erythroblast proliferation and differentiation. Upon EPO stimulation, EPOR dimerizes triggering the JAKZ/STATS signaling cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-mediated signals.
-!- SUBGNIT: Interacts with APS.
-!- SUBGNIT: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY.CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH BPO. MEDLINE=98446092; PubMed=9774108; Syed R.S., Reid S.W., Li C., Cheetham J.C., Aoki K.H., Liu B., Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J., Elliott S., Sitney K., Katz B.A., Matthews D.J., Wendoloski J.J., Egrie J., Stroud R.M.; Fatz B.A., Matthews D.J., Wendoloski J.J., "Efficiency of signalling through cytokine receptors depends critically on receptor orientation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.40 ANGSTROMS) OF 34-246.
MEDLINE=99141272; PubMed=9974392;
Livnah O., Stura E.A., Middleton S.A., Johnson D.L., Jolliffe L.K.,
Wilson I.A.;
                                                                                                                                                                                                                            MEDLINE=99023198, PubMed=9808045;
MEDLINE=99023198, PubMed=9808045;
Livnah O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,
Jolliffe L.K., Wilson I.A., He W., Krause C.D., Pestka S.,
Jolliffe L.K., Wilson I.A.,

"An artagonist peptide-EPO receptor complex suggests that receptor
dimerization is not sufficient for activation.";

Nat. Struct. Biol. 5:993-1004(1998).
                                                                   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.
MEDLINE=56291992, PubMed=8662530,
Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulcahy L.S.,
Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.,
Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.,
Experience of a protein hormone by a peptide agonist: the
EPO receptor complex at 2.8 A.";
Science 273:464-471(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO:0005887; C:integral to plasma membrane; TAS. GO:0004900; F:erythropoletin receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subfamily 1. SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002996; CRIA:
InterPro; IPR008957; FN_III-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M34986; AAAS2401.1; -.
EMBL; M60459; AAAS2403.1; -.
EMBL; S45332; AAB23371.1; -.
EMBL; M76595; AAAS2393.1; -.
EMBL; M77344; AAAS2392.1; -.
PIR; A43799; ZUHUR.
                      collaboration with c-Cbl.";
Leukemia 13:760-767(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; IEBP; 29-UUL-97.
PDB; IEBA; 18-NOV-98.
PDB; IERR; 01-COT-99.
PDB; ICNA; 11-AUG-99.
PDB; IERN; 07-JAN-00.
Genew; HGNC:3416; EPOR.
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Gaps

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507 AA

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Punctional erythropoietin receptor of the cells with neural characteristics. Comparison with receptor properties of erythroid
                                                                                                                                                                                                                           Pfam; PF00041; fn3; 1.
PIRSP; PIRSF001959; BPO_receptor; 1.
SMART; SM00060; FN3; 1.
PROSITE; PS01352; HRWATOPO REC_L_F1; 1.
Receptor; Transmembrane; GTycoprotein; Signal; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APS-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL
E -> D (IN REF. 3; AAR20029).
W; 067657AZE26451CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91266574; PubMed-7684373;
Masuda S., Nagao M., Takahata K., Konishi Y., Gallyas F.,
Tabira T., Sasaki R.;
                                                                                                                                                                                                                                                                                                                                                         ERYTHROPOIBTIN RECEPTOR. EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 109; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
18-FARR-2004 (Rel. 43, Last annotation update)
Brythropoletin receptor precursor (BPO-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                           InterPro; IPR002996; CRIA.
InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR003528; Hemtopoptn_L_Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 QRVEVLEGRIECVLSNLRGGTRY 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55194 MW;
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21; Conservative
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M62360; AAA37572.1;
M62360; AAA37582.1;
S59388; AAB20029.2;
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272
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367
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106
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291
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                                                            PIR, A41686; A32385.
PIR, S14081, S14081.
HSSP; P19235; IEBA.
                                                                                                                            MGD; MGI:95408; Epor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
507 AA;
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Best Local Similarity
Matches 21; Conserv
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BPOR_RAT
ID _EPOR_RAT
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Miura O., Cleveland J.L., Ihle J.N.;
Miura O., Cleveland J.L., Ihle J.N.;
Miura O., Cleveland J.L., Ihle J.N.;
Minactivation of erythropoietin receptor function by point mutations in a region having homology with other cytokine receptors.";
Mol. Cell. Biol. 13:1788-1795(1993).
-! FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-induced erythroblast proliferation and differentiation. Upon EPO stimulation, EPOR dimerizes triggering the JAK2/STATS signaling cascade. Isoform 2 acts as a dominant-negative receptor of EPOR-mediated signals.
-!- SUBCKLULAR LOCATION: Type I membrane protein.
-!- SUBCKLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The adapter protein APS associates with the multifunctional docking sites Tyr-568 and Tyr-936 in c-Kit."; Biochem. J. 370:1033-1038(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-24 FROM N.A.
SEQUENCE OF 1-24 FROM N.A.
MEDLINE=91201346; PubMed=1849897;
Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H.,
Gisselbrecht S., Cartron J.-P.;
"Spleen focus-forming virus long terminal repeat insertional
activation of the murine erythropoietin receptor gene in the T3Cl-2
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92017832; PubMed=1656233;
Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;
Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;
"Unregulated expression of the erythropoietin receptor gene caused insertion of spleen focus-forming virus long terminal repeat in a murine erythroleukemia cell line.";
Mol. Cell. Biol. 11:5527-5533 [1991].
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-27 FROM N.A.
BEDLINES-90287158 PubMed-2162479;
Youssoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;
"Structure and transcription of the mouse erythropoietin receptor
                                                                                                                 SECURNCE FROM N.A.
STRAIN=BALB/c; TISSUE=Liver;
STRAIN=91080149; PubMed=2175360;
Kuramochi S., Ikawa Y., Todokoro K.;
"Characterization of murine erythropoietin receptor genes.";
[3] Mol. Biol. 216:567-575(1990).
                 SEQUENCE FROM N.A.
MEDLINE-81195218; PubMed=2539263;
D'Andrea A.D., Lodish H.F., Wong G.G.;
Expression cloning of the murine erythropoietin receptor.";
Cell 57:277-285(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22510236; Pubmed=12444928;
Wollberg P., Lennarteson J., Gottfridsson E., Yoshimura A.,
Ronnstrand L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subfamily 1. SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell. Biol. 10:3675-3682(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 266:6952-6956(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; J04843; AAA37571.1; -. EMBL; X53081; CAA37248.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukemia cell line.
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MUTAGENESIS.

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Gaps

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1; Indels

507 AA

Length 507;

(POTENTIAL)

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation induced earthroblast proliferation and differentiation. Upon BPO stimulation, BPOR dimerizes tridgering the JAKZ/SIATS signaling cascade. Isoform 2 acts as a dominant-negative receptor of BPOR-mediated signal.

-1. SUBGELIUMAR LOCATION: Type I membrane protein.
-1. SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.
-1- SIMILARITY: Contains 1 fibronectin type III domain. cells."; J. Biol. Chem. 268:11208-11216(1993).

3. 3.

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or send an email to license@isb-sib.ch)
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Q99N43;
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                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MBDLINB=22229977; PubMed=12381787;
MBDLINB=2229977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14427 (2002).
-:- FUNCTION: Probable Sci. G.-Amechionine dependent methyltransferase specific for a sterol and/or lipid substrate (By
        There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                             Or bc.

EMBL, D13566; BAAC.

EMBL, D13566; BAAC.

EMBL, D13566; BAAC.

R InterPro; IRR002956; CRIA.

A InterPro; IRR003961; FW III-like.

DR InterPro; IRR003961; FW III.

DR InterPro; IRR003961; FW III.

DR InterPro; IRR003961; FW III.

DR PRSF; SMO0606; FW3; 1.

DR PROSITE; PS01352; HEMATOPO REC L F1; 1.

DR Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL

SIGNAL

25 249 EXTRACELULAR (POTENTIAL).

CHAIN

25 249 EXTRACELULAR.

POTENTIALD.

SOO CYTOPLASHIC (POTENTIAL).

FIRROWECTIN TYPE-III.

"" SIGNAL

SOO CYTOPLASHIC.

"" SIGNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (POTENTIAL).
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last semocation update)
Methyltransferase gidB (EC 2.1.-.-) (Glucose inhibited division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109; DB 1; Length 507;
Pred. No. 1.5e-09;
1; Mismatches -1; Indels
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-!- SIMILARITY: Belongs to the gidB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
        European Bioinformatics Institute.
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91.3%;
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GIDB OR BL0646.
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Q8G6J4;
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GIDB_BIFLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ringle-containing transmembrane protein.;

Kringle-containing transmembrane protein.;

Biochim. Biophys. Acta 1518:63-73(2001).

L. FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Wht/Deta-catenin signaling (By similarity).

L. ISSUB SERCIFICITY: In the adult, wielely expressed with high levels in heart, lung, kidney, skeletal muscle and testis.

L. DEVELOPMENTAL STAGE: In the embryo, expression is first detected on day 9 and increases up to day 18. Lower levels are found in adult. At 9.5 dpc, expression is localised to the apical ectodermal ridge (ARR) of the developing fore- and hindlimb buds, the telencephalon and the first brachial arch. At 10.5 dpc, expression is also observed in the myotome and in sensory tissues such as the nasal pit and optic vesicle.

SIMILARITY: Contains 1 KWSC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Kremen protein i precursor (Kringle-containing protein marking the eye
and the nose) (Dickkopf receptor).
KREMENIO R KREMEN
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY TISSUE=Prain, and Kidney;
MEDLINE=21167372; PubMed=11267660;
MARAMURA T., Aoki S., Kirajima K., Takahashi T., Matsumoto K.,
                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and characterization of Kremen, a novel
                                                                                                                                                                                                                                                                                         Length 221;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                            TIGREAMS; TIGRO0138; gidB; 1.
Transferase; Methyltransferase; Complete proteome.
SEQUENCE 221 AA; 24163 MW; FB131A5126368A05 CRC64;
                                                                                                                                                                                                                                                                                            Score 49; DB 1;
Pred. No. 1.8;
5; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00747; ICEA.
MGD, MGI:1933988; Kremen.
GO; GO:0016021; C:integral to membrane; NAS.
InterPro; IPR000859; CUB.
InterPro; IPR000001; Kringle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
EMBL; AE014686; AAN24468.1;
                               HAMAP; MF 00074; -; 1.
InterPro; IPR003682; GidB.
Pfam; PF02527; GidB; 1.
ProDom; PD00441; GidB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Nature
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Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Mutakawa K., Kanehori K., Takahashi-Pujii A., Oshima A., Sugiyama A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBDLINB=20057165; PubMed=10591208; Dunham I., Hunt A.R., Collins V.E., Bruskiewich R., Babbage D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Bagguley C., Bailey J., Barlow K.P., Bates K.N., Beasley O.P.,
                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.9%; Score 49; DB 1; Length 473; 55.0%; Pred. No. 4.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nakamura T., Nakamura T.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isogai T.;
"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                 Transmembrane, Kringle.
                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL). KRINGLE.
                                                                                                                                                                                                                                  KREMEN PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.1
                                                                                                                                   PROSITE; PS01180; CUB; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
WHO Signaling pathway; Signal; Transmen SIGNAL
                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 VELLDGYTHRVLVRLSGRSR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VEILEGRIECVLSNLRGRIR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                               Pfam; PF00051; kringle; 1.
Pfam; PF01822; WSC; 1.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SWART; SW0012; CUB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51716 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 : 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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CARBOHYD
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DT 28-FEB.
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BETTE C.P. BIRATO S.E. Bridgeman A.M., Buck D., Burgess Jirk G., Concoller W. S., Connor P. S., Connor P. C., Concoller W. S., Connor P. S., Connor P. S., Connor P. C., Concoller W. S., Connor P. S., Connor P. S., Connor P. C., Concoller W. S., Connor P. C., Concoller W. S., Connor P. C., David M. D., Mall C., Bland P.D., Corche W. W., Coville G.J., Concoller W. S., Connor P. C., Bland P.D., Concoller W. S., Connor P. S., Connor P. S., Connor P. S., Bland P.D., Concoller W. S., Connor P. S., Bland P. S., Bl
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us-10-612-885a-1.rsp

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IIGRFAMS; TIGRO0670; asp_carb_tr; 1.
                                                                                                                                                                                                            Best Local Similarity
Matches 11; Conserv
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PYRB CORGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 13:1572-1579(2003).
-ı- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
VSD -> AIQDSEVTSLIWSQGQPRSI (in 180form
                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Comparative complete genome sequence analysis of the amino acid replacements responsible for the thermostability of Corynebacterium efficiens.";
                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura B., Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K., Gojobori T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corymebacterineae; Corymebacteriaceae; Corymebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                    Score 49; DB 1; Length 475;
Pred. No. 4.1;
                     PRINTS; PRO0018; KRINGLE.
ProDom; PRO0018; KRINGLE.
SMART; SM00042; CUB; 1.
SMART; SM00130; KR; 1.
PROSITE; PS01018; KRINGLE 1; 1.
PROSITE; PS0070; KRINGLE 1; 1.
PROSITE; PS0070; KRINGLE 2; 1.
MAR Eignaling pathway; Signal; Transmembrane; Kringle; Alternative splicing.
SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
transcarbamylase) (ATCase).
                                                                                                                                                                                                                                                                               30 MISSING (IN REF. 1).
206 I -> V (IN REF. 2).
51898 MW; B7E86FD80F96A0A4 CRC64;
                                                                                                                           KREMEN PROTEIN 1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + N-carbamoyl-L-aspartate.
-!- PATHWAY: Pyrimidine biosynthesis; second step.
-!- SIMILARITY: Belongs to the ATCase/OTCase family.
                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
KRINGLE.
                                                                                                                                                                                                                                    (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
MEDLINE=22723752; PubMed=12840036;
                                                                                                                                                                                                                                                                         .003500
                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                         (GLCNAC
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4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              312 AA
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N-LINKED
N-LINKED
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                                                                                                                                                                                                      N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                        270 VELLDGYTHRVLARFHGRSR 289
                                                                                                                                                                                                                                                                                                                                                             3 VEILEGRIECVLSNLRGRIR 22
                                                                                                                                                                                                                                                                                                                       41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corynebacterium efficiens
          Pfam; PF00051; kringle; 1. Pfam; PF01822; WSC; 1.
                                                                                                                                                                                                                                                                                                                                 Local Similarity 50.0
les 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
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VARSPLIC
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Q8FT39;
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC, ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate + N-carbamoyl-L-aspartate.
-!- PATHWAY: Pyrimidine biosynthesis; second step.
-!- SIMILARITY: Belongs to the ATCase/OTCase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%; Score 48; DB 1; Length 312;
61.1%; Pred. No. 3.7;
ive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrimidine biosynthesis; Transferase; Complete proteome.
SEQUENCE 312 AA; 33706 MW; EEF40AAD98413D3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8NQJ8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Aspartate carbamcyltransferase (EC 2.1.3.2) (Aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 AA
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STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMB; TIGR00670; asp carb tr; 1.
PROSITE; PS00097; CARBAMOYLITANSFERASE; 1.
                                                                                                                                                                                                                                                                                                      HAMAP; MF_00001; -; 1.
InterPro; IRR006130; App/Orn_COtranf.
InterPro; IRR006130; App_carbmitransf.
InterPro; IRR006131; OrCace_0.
InterPro; IRR006132; OrCace_P.
Pfam; PR00185; OrCace; 1.
Pfam; PR01875; OrCace; 1.
Pfam; PR01875; ACCACE N; 1.
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InterPro; IPR006130; Asp/Orn_COtranf.
InterPro; IPR002082; Asp_carbmltransf.
InterPro; IPR006131; OfCace_O.
InterPro; IPR006132; OfCace_P.
                                                                                                                                                                                                                                                             EMBL; AP005219; BAC18542.1; ALT_INIT.
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EVLEGREVKKLPTLRGRT
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PYRB OR CGL1612.
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Pfam; PF02729; OTCace N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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DOMAIN
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TISSUE-Retina,

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

A Strausberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carawant T.L., Scheetz T.E.,

Brownstein M.J., Uedin T.B., Toshiywik S., Carninoi B., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gabb R.A.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R Hunn and mouse CDNA sequences "." Nor Young A. G. Schnert B.A.,

R Denre A., Schein J.E., Jones S.J.M., Marra M.A.,

R Denre A., Schein J.E., Jones S.J.M., Marra M.A.,

R Denre A., Schein J.E., Jones S.J.M., Marra M.A.,

R Denre A., Schein J.E., Panger R.B.,

R Denre A., Schein J.E., Panger R.B.,

R Denre A., Schein J.E., Jones S.J.M., Marra M.A.,

R Denre A., Schein J.E., Panger R.B.,

R Denre A., Rein J. R. R. Q. Q. School Full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-736 FROM N.A.
MEDLINE=97474796; PubMed=9331372;
Winfield S.L., Tayebi N., Martin B.M., Ginns B.I., Sidransky E.;
"Identification of three additional genes contiguous to the
glucocerebrosidase locus on chromosome 1q21: implications for Gaucher disease.";
                                                                               Gape
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-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=96044440; PubMed=7558000;
Adolph K.W., Long G.L., Winfield S., Ginns B.I., Bornstein P.,
"Structure and organization of the human thrombospondin 3 gene
                                                 Query Match
41.0%; Score 48; DB 1; Length 312;
Best Local Similarity 61.1%; Pred. No. 3.7;
Matches 11; Conservative 1; Mismatches 6; Indels
              Pyrimidine biosynthesis; Transferase; Complete proteome. SEQUENCE 312 AA; 33894 MW; F33154F4D033CF22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P49746; QBWV34;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Thrombospondin 3 precursor.
                                                                                                                                                                                                    956 AA
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1
                                                                                                       21
                                                                                                                     27 EVLEGREVKKLPTLRGRT 44
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                                                                                                       4 EILEGRIECVLSNLRGRI
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                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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EMBL; X69582; CAA49296.1; -.
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Best Local Similarity 42.9
Matches 9; Conservative
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STANDARD;
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                                                                                                                                    NCBI TaxID=28985;
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 RS28 KLULA
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RS28 KLUMA
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                                                                                                                                                                                                                                                                                                                                          Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITRE-22550857, PubMed=12663927;
Pauleen I.T. Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R., Read T.D., Pouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F., Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M., Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W. Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H., Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M., "Role of mobile DNA in the evolution of vancomycin-resistant
              310 N-LINKED (GLCNAC. . .) (POTENTIAL).
407 N-LINKED (GLCNAC. . .) (POTENTIAL).
644 N-LINKED (GLCNAC. . .) (POTENTIAL).
317 N-LINKED (GLCNAC. . .) (POTENTIAL).
104201 NW; AESB136DF0FFESB8 CRC64;
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FAE19A0C5D93CE4E CRC64;
                                                                                                40.2%; Score 47; DB 1; Length 956; 45.5%; Pred. No. 18; 1ive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 1; Length 58;
Pred. No. 1.2;
4; Mismatches 2; Indels
  BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 299:2071-2074(2003).
-!- SIMILARITY: Belongs to the tautomerase family.
                                                                                                                                                                                                                                                                                10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0bable tautomerase EF2859 (EC 5.3.2.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
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ProDom; PD404143; Taut; 1.
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VELIEGRTEEQLTNM 19
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STRAIN=V583 / ATCC 700802;
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HAMAP; MF_00718; -; 1.
InterPro; IPR004370; Taut.
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Query Match
Best Local Similarity 60.0
Matches 9; Conservative
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les 10; Conservative
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       936
310
407
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956 AA;
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RESULT 11 RS28_KLULA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDAMED 1481571; MEDITHS 93127729; PubMed=1481571; MEDLINE=93127729; PubMed=1481571; Meckstar R., Ferreira P.M., Bootsman T.C., Mager W.H., Planta R.J.; "Structure and expression of the ABF1-regulated ribosomal protein S33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Yeast 8:949-959(1992).
-1- SIMILARITY: Belongs to the S28E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                               gene in Kluyveromyces.";
Yeast 8:949-959(1992).
-i- SIMILARITY: Belongs to the S28B family of ribosomal proteins.
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Bukarycta; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                      Kluyveromyces lactis (Yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.3%; Score 46; DB 1; 42.9%; Pred. No. 1.4; tive 4; Mismatches E
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
40S ribosomal protein S28 (533).
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DRC-1998 (Rel. 37, Last annotation update)
408 ribosomal protein S28 (S33).
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InterPro; IPR001289; Ribosomal S28e.
Pfam: PF01200; Ribosomal S28e; I.
ProDom; PD005541; Ribosomal S28e; I.
PROSITE; PS00961; RIBOSOMAL S28E; I.
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MEDLINE=93127729; PubMed=1481571;
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SPECIES=M.tuberculosis, STRAIN=H37Rv;

MEDLINE=98295987, PubMed=9634230;

A Gold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Badcock K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

Oliver S., Geborne J., Quail M.A., Rajandream M.A., Rogers J.,

Rutter S., Seeger K., Skelton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

T. "Deciphering the biology of Mycobacterium tuberculosis from the

complete genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SPECISE=M. tuberculosis, STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Ple1schmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Rollonay J.F., Nelson W.C., Umayam L.A., Ernolaeva M., Salzberg S.L.,
Bishai W., Jacobs W.R. Jr., Weidman J., Khouri H., Gill J., Mikula A.,
Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.bovis; STRAIN=AF2122/97; MEDLINE=22709107; PubMed=12788972; MEDLINE=22709107; PubMed=12788972; Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H., Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Colle S.T., Gordon S.V., Hewinson R.G.; The complete genome sequence of Mycobacterium bovis."; Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                              39.3%; Score 46; DB 1; Length 67; 42.9%; Pred. No. 1.4;
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative eytochrome P450 128 (EC 1.14.--).
CYP128 OR RV2268C OR MT2330 OR MTCY339.42 OR MB2291C.
Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                 Ribosomal protein.
SEOUENCE 67 AA; 7522 MW; B1E558353F18A131 CRC64;
modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                        EMBL, X69583; CAA49297.1; -.
PIR, S30006; S30006.
InterPro, IPR000289; Ribosomal S28e.
Probom, PP01200; Ribosomal S28e; 1.
Probom, PD005541; Ribosomal S28e; 1.
PROSITE; PS00961; RIBOSOMAL_S28E; 1.
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    Bacteriol. 184:5479-5490(2002)

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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculier, Rv2268c, -.
InterPro; IPR001128, Cytochrome_P450.
InterPro; IPR001128, Cytochrome_P450.
PRIMTS; PR00365, P450.
PROSITE; PS00086; CYTOCHROME_P450, 1.
Hypothetical protein; Oxidoreductase; Monooxygenase; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.3%; Score 46; DB 1; Length 489; 47.6%; Pred. No. 13; tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRON (HEME AXIAL LIGAND) (BY 633F233CBF03AD7A CRC64;
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
AMS2 OR SPCC290.04 OR SPCG4F11.01
Schizosaccharomyces pombe (F18sion yeast).
Schizosaccharomycetales; Schizosaccharomycetes; Schizosaccharomycetaes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       697 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
POTENTIAL.
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458 RIBUVEPPTWTTNANLRGLTR 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RVEILEGRTECVLSNIRGRTR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BX248342; CAD97152.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53313 MW;
                                                                                                                                                                                                                                                                                                                                                            EMBL; Z77163; CAB00967.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.6
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 4
489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; H70729; H70729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
TRANSMEM 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
AMS2_SCHPO
ID _AMS2_SCHPO
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Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., Thode G., Shpakovski G.V., Barrell B.G., Nurse P., Harst S.L., The genome sequence of Schizosaccharomyces pombe.",
                                                                                                                                                                                                                                          FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
MEDLINE=22423783; PubMed=12535531;
Chen E.S., Saltoh S., Yanagida M., Takahashi K.;
Chen E.S., Saltoh S., Yanagida M., Takahashi K.;
Chen E.S., Saltoh S., Yanagida M., Takahashi K.;
Of CENP-A in fission yeast.",
Mol. Cell 11:175-187 (2003).
-! FUNCTION: Required for proper chromosome segregation via
regulation of CENP-A localization to the centromere.
-! SUBGNIT: Interacts with CENP-A.
-! SUBGLILLULAR LOCATION: Nuclear; centromeric.
-! SIMILARITY: Contains 1 GATA-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00344; GATA ZN FINGER 1; FALSE NEG.
PROSITE; PS50114; GATA ZN FINGER 2; 1.
Transcription regulation; Nuclear protein; Centromere; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.3%; Score 46; DB 1; Length 697; 40.9%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 GATA-TYPE (ATYPICAL).
78159 MW; 37E68D8232C1C069 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein F44E2.4 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312 BOVRIARGRIEKKFTNVRGKNR 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenebB SPombe; SPCC290.04; -. GO; GO:0005694; C:chromosome; ISS. GO; GO:0005654; C:chromosome; ISS. GO; GO:0005654; C:chucleoplasm; ISS. GO; GO:0007049; P:cell cycle; ISS. InterPro; IPR000679; Znf GATA. SMART; SM00401; ZnF GATA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ORVEILEGRIECVLSNLRGRIR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AL035260; CAB61504.1; -. EMBL; AL117389; CAB55767.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 3
697 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                          Coulson A.
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownken I
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                      "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 1609 AA; 175966 MW; 4AE845E2AD2207CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 1;
Pred. No. 47;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    completed: May 6, 2004, 12:45:26
                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
-!- SIMILARITY: TO HUMAN KIAA0152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P01130; 1AJJ.
Wormbep, F94E2.4; CE00182.
Pfam, PF00057; Idl recept_a; 1.
SMART, SMO0192; LDLa; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L23646; AAA28040.1; -.
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877 LLEGRISCVVSS 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 ILEGRIECVISN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S44821; S44821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: Nob time: 12 secs
                                                                                                                                                                                                            Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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version 5.1.6
- 2004 Compugen Ltd.
GenCore (c) 1993
         Copyright
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- protein search, using sw model OM protein

May 6, 2004, 12:44:02 ; Search time 21 Seconds (without alignments) 105.353 Million cell updates/sec Run on:

1 QRVEILEGRIECVLSNLRGRIRY 23 US-10-612-885A-1 117 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * 78:* PIR Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	,	Description	erythropoietin rec		erythropoletin rec	erythropoietin rec		ribosomal protein	ribosomal protein	Ω	cytochrome P450 Rv	probable transcrip	F44E2.4 protein -	ATP-dependent RNA	probable transmemb	hypothetical prote	axonin 1 precursor	protein PV100 [imp		hypothetical prote	н	hypothetical profe	IS1167, transposas	IS1167, transposas	μ	д		probable protein-t		protein-tyrosine-p	protein-tyrosine-p
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		8	ZUHUR	S14081	A32385	A46713	A57121	830006	830005	T30648	H70729	T41352	S44821	\$42639	D83406	D70506	S22383	T44430	AB0673	AE1823	C97995	A87649	C95184	F95096	S76870	S66574	A46016	T31093	H71251	46	A56178
		8	-	~	Н	Н	~	~	~	~	Н	~	~	ч	7	н	~	~	~	~	~	~	~	~	~	~		N	~	~	0
		Match Length	508	265	507	507	926	67	67	288	489	710	1609	607	316	512	1036	810	47	195	84	408	н	-	654	931	LD.	1437	228	83	1912
do	Query	Match	100.0		93.2	93.2		39.3		39.3	39.3	σ	39.3	38.9	38.5	38.5	38.5	38.0		7	36.8	ø	36.8	36.8			36.8	•	36.3	36.3	36.3
		Score	117	109	109	109		46	46	46	46	46	46	45.5		45	45	44.5	44	44	43	43	43	43	43	43	43	43		42.5	42.5
	lesult	No.	-	7	m	4	2	9	7	60	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23		25				53

ribosomal protein	ribosomal protein	hypothetical prote	transposase (orf2)	degenerate transpo	esterase slr1916 -	hypothetical prote	aspartate-semialde	IS1167, transposas		-	IS1167, transposas				hydrogenase regula
R3BY33	S51401	T49830	A97877	C98084	875226	D89785	300198	A95168	B95197	E95146	H95208	T46944	AI0554	T29652	E70399
н	~	~	~	~	N	~	~	~	~	~	~	~	~	~	CN,
67	67	231	255	260	283	322	365	418	418	418	418	482	482	514	562
35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9	35.9
42	42	42	42	42	4,	42	42	42	42	42	42	42	42	42	42
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

П	
SULT	HUR

erythropoietin receptor precursor - human

CiAccession: A47799; #8equence revision 05-Apr-1995 #text change 22-Jun-1999 CiAccession: A47799; A60160; A48824; A53958; A55280; I52563 F.Yones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G. Blood 76, 31-35, 1990 A.D.; Haines, L.L.; Wong, G.G. A;Title: Human erythropoietin receptor: cloning, expression, and biologic characterizat A;Reference number: A43799; MUID:90304340; PMID:2163696 A;Molownia, A43799

A;Molecule type: mRNA A;Residues: 1-508 < JON A;Residues: 1-508 < JON A;Crose-references: GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245 A;Crose-references: GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245 B;Mincelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B. Blood 76, 24-30, 1990 Bjood 76, 24-30, 1990 A;Aitle: The gene for the human erythropoietin receptor: analysis of the coding sequenc A;Reference number: A60160; WUID:90304334; PMID:2163695

;Status: not compared with conceptual translation

A;Molecule type: mRNA; DNA A;Residues: 1-101, "K', 103-188, "RP', 191-243, "E', 245-508 <WIN> A;Residues: 1-101, "K', 103-188, "RP', 191-243, "E', 245-508 <WIN> A;Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D. Blood 78, 2548-2556, 1991 A;Title: Cloning of the human erythropoietin receptor gene. A;Reference number: A49824; MUID:92399733; PMID:1668606

A,Residues: 1.508 <NOG> A,Korse-references: GB:845332, NID:g255496; PIDN:AAB23271.1; PID:g255497 A,Experimental source: placenta A,Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIP:113294)

;Shrenman, K.; St. John, T. xp. Hematol. 19, 973-977, 1991 ;Title: The erythropolatin receptor gene: cloning and identification of multiple trans ;Reference number: A53958; MUID:91372359; PMID:1654273

Molecule type: mRNA;Residues: 1-508 <EHR>

RiPenny, L.A.; Forget, B.G. Genomics 11, 974-980, 1991 A.Title: Genomic organization of the human erythropoletin receptor gene. A;Reference number: A55280, WUID:92147143; PMID:1664413

A; Molecule type: DNA A; Molecule type: 1-17; 381-387, 'LLEQQQDA', 391-395; 504-508 cPEN> A; Molecule and the modal fied after extraction from NCBI backbone A; Note: the authors translated the codon GAT for residue 31 as B A; Note: an insert compared to other published sequences is considered by authors as liken and insert compared to other published sequences is considered by authors as liken and NA Molecules L:; Tournamille, C:; Hattab, C:; Boffa, G:; Cartron, J.P.; Chretien, S. Blood 78, 2557-2563, 1991
A; Title: Cloning of the gene encoding the human erythropoietin receptor.

```
erythropoietin receptor precursor - rat
Cispecies: Rattus norvegicus (Norway rat)
Cjate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
CjAccession: A46713
R;Masuda, S; Nagao, M; Takahara, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki
A; Biol. Chem. 268, 11208-11216, 1993
A;Title: Functional erythropoietin receptor of the cells with neural characteristics. C
A;Reference number: A46713; MUID:93266574; PMID:7684373
    RiHino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A;Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A;Reference number: A41686; MUID:92017832; PMID:1656233
A;Accession: A41686
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A,Cross-references: GB:D13566; NID:g286209; PIDN:BAA02761.1; PID:g286210
A,Note: sequence extracted from NGB1 backbone (NCBIN:132811, NCBIP:132813)
A,Note: sequence extracted from NGB1 backbone (NCBIN:132811, NCBIP:132813)
C,Superfamily: erythropoietin receptor; cytokine receptor homology
C,Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted cAIGs-
F;25-307/Product: erythropoietin receptor #status predicted cAIGs-
F;25-349/Domain: extracellular #status predicted cAITs-
F;52-348/Domain: cytokine receptor homology cCRS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-507 cDAA>
A;Residues: 1-507 cDAA>
A;Residues: 1-507 cDAA>
A;Residues: 1-507 cDAA>
A;Experimental source: murine erythroleukemia (MEL) cells, subclone 745
A;Experimental source: murine erythroleukemia (MEL) cells, subclone 745
R;Kuramcohli, S; Ikawa, Y.; Todokoro, K.
A;Mol. Biol. 216, 567-575, 1990
A;Mitle: Characterization of murine erythropoietin receptor genes.
A;Mitle: Characterization of murine erythropoietin receptor genes.
A;Reference number: S13249; MUID:91080149; PMID:2175360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-507 <KUR>
Cross-references: EMBL:XS3081; NID:950861; PIDN:CAA37248.1; PID:950862
Experimental source: murine erythroleukemia K-1 cells
                                                                                                                                                                                                                                                                                                                          A; Residues: 1.507 AIN>
A; Residues: 1.507 AIN>
A; Cross-references: GB:S59388; NID:g237036; PIDN:AAB20029.1; PID:g237037
A; Cross-references: GB:S59388; NID:g237036; GEL]
B; D; Andrea, A.D.; Lodish, H.F.; Wong, G.G.
R; D; Andrea, A.D.; Lodish, H.F.; Wong, G.G.
A; 277-285; J889
A; Title: Expression cloning of the murine erythropoietin receptor.
A; Reference number: A32385; MUID:89195238; PMID:2539263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3; Superfamily: erythropoietin receptor; cytokine receptor homology skywodia alternative splicing; cytokine receptor; glycoprotein; 1-24/Domain: signal sequence #status predicted <SIG>.25-507/Product: erythropoietin receptor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;25-249/Domain: extracellular #status predicted <EXT>
F;52-238/Domain: cytokine receptor homology <CRS>
F;520-271/Domain: transmembrane #status predicted <TMM>
F;272-507/Domain: intracellular #status predicted <INT>
F;272-50,90-106/Disulfide bonds: #status predicted <INT>
F;52-62,90-106/Disulfide bonds: #status predicted
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 1; Length 507; Pred. No. 4.6e-09; 1; Mismatches 1; Indels
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Best Local Similarity 91.3
Matches 21; Conservative
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A;Residues: 1-507 <MAS>
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                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
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A/Map position: 19p13.3-19p13.2

C/Map position: 19p13.3-19p13.2

C/Map position: 19p13.3-19p13.2

C/Map position: 19p13.3-19p13.3

C/Map position: 19p13.3-19p13.3

C/Map position: 19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13.3-19p13
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A,Rolecule type: DNA
A,Residues: 1-265 «KUR»
A,Residues: 1-265 «KUR»
A,Residues: 1-265 «KUR»
B,iacombe, C.; Chretten, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.
J. Blol. Chem. 266, 6952-6956, 1991
A,Title: Spleen focus-forming virus long terminal repeat insertional activation of the RA,Reference number: 149653; MUID:91201346; PMID:1849897
A,Reference number: 149653
A,Residues: 1-24 «RES»
A,Residues: 1-24 «RES»
A,Residues: 1-24 «RES»
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C;Species: Mus musculus (house mouse)
C;Accession: 18-Peb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S14081; 149653
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A;Fitle: Characterization of murine erythropoietin receptor genes.
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C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999
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C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: cytokine receptor; transmembrane protein
F;52-238/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                                     A; Cross-references: GB: M76595; NID: 9182147; PIDN: AAA52393.1; PID: 9553281
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Fi273-509/Domain: intracellular #status predicted <INT>
Fi50-62,91-107/Disulfide bonds: #status predicted
Fi76/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Reference number: 152563; MUID: 92399734; PMID: 1668607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 QRVEILEGRIECVLSNLRGRIRY 216
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                                                                               A;Status: translated from GB/EMBL/DDBJA;Molecule type: DNA
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Matches 21; Conserv
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Best Local
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Veast 8, 949-959, 1992
A:Title: Structure and expression of the ABF1-regulated ribosomal protein S33 gene in K.
A:Reference number: S30005; MUID:93127729; PMID:1481571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
;Accession: S30005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable DNA-binding protein 46L - Molluscum contagiosum virus 1
N;Alternate names: MCO46L
C;Species: Molluscum contagiosum virus 1
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 27-Oct-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J
                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein S28.e - yeast (Kluyveromyces marxianus var. lactis)
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39.3%; Score 46; DB 2; Length 288;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 2; Indels
                                                                                               2; Length 67;
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                                                                                                                                                     Indels
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Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: T30648
Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                            Score 46; DB;
Pred. No. 3.7;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB
Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Gene: S33
C;Superfamily: rat ribosomal protein S28
C;Keywords: protein biosynthesis; ribosome
        C,Superfamily: rat ribosomal protein S28
C,Keywords: protein biosynthesis, ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                         Alternate names: ribosomal protein YS33
                                                                                                                                                                                                   2 RVEILEGRIECVLSNLRGRIR 22
                                                                                                                                                                                                                                         29 RVEFLEDITRIJVRNVKGPVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RVEILEGRIECVLSNLRGRIR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 RVEFLEDTTRIVRNVKGPVR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                         Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: S53420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ECVLSNLRGRTR 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-288 <SEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-67 <HOE>
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H70729
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./Title: Structure and expression of the ABF1-regulated ribosomal protein S33 gene in Kl
./Reference number: S30005; MUID:93127729; PMID:1481571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: mRNA; Reddues: 1-956 <ADD.; Pilosepse PIDN: AAC41762.1; PID: 9886299; GB: L38970; Residues: 1-956 <ADD.; Pilosepse Pilosepse PIDN: AAC41762.1; PID: 9886299; GB: L38970; Minfield, S.L.; Tayebi, N.; Martin, B.M.; Ginns, E.I.; Sidransky; B. enome Res. 7, 1020-1026, 1997 and pane Res. 7, 1020-1026; 1997; Fiftle: Identification of three additional genes contiguous to the glucocerebrosidase; Reference number: 216482; MUID: 97474796; PMID: 9331372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Map position: 1q21-1q23
:Introns: 27/1; 96/1; 181/3; 216/1; 225/1; 256/1; 270/1; 319/3; 366/3; 392/3; 443/3;
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                                                                                                                                                                                                                                                                                                                                                                                                             thrombospondin 3 precursor - human
C;Species: Homo sapiens (man)
C;Date: 03-NOv-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Date: 03-NOv-1995; #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: A5-1013; #0.1995
Genomics 27, 329-336, 1995
A;Title: Structure and organization of the human thrombospondin 3 gene (THBS3).
A;Reference number: A57121; MUID:96044440; PMID:7558000
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Residues: 1-736 <WIN>
Cross-references: EMBL:AF023268; NID:g2564910; PIDN:AAC51818.1; PID:g2564912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosomal protein S28.e - yeast (Kluyveromyces marxianus)
N/Alternate names: ribosomal protein YS33
C;Species: Kluyveromyces marxianus
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: mediates cell-to-matrix and cell-to-cell interactions C;Superfamily: thrombospondin 3; EGF homology F;374-412/Domain: EGF homology <EGF>
                                                                                                                                                                          ö
F;250-271/Domain: transmembrane #status predicted <TWM>
F;272-507/Domain: intracellular #status predicted <INT>
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                             Score 109; DB 1; Length 507;
Pred. No. 4.6e-09;
1; Mismatches 1; Indels
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40.2%; Score 47; DB 2;
Best Local Similarity 45.5%; Pred. No. 41;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GDB:409953; OMIM:188062
                                                                                                                                                                                                                                                    193 QRVEVLEGRIECVLSNLRGGTRY 215
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OOAGLADGRTHTVLLRLRGPSR 134
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                                                                                                          Query Match 93.2%;
Best Local Similarity 91.3%;
Matches 21; Conservative
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Residues: 1-67 <HOE>
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probable transmembrane sensor PA1911 [imported] - Pseudomonas aeruginosa (strain PA01) cipaceies: Pseudomonas aeruginosa (cjpaceies: Pseudomonas aeruginosa PA01, ar hickey, M.J.; Brady, S.; Olson, M.V. (coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. (coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. (coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. (coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lim, J.; M.J.; M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arpendent RNA helicase DB10 - wood tobacco (Species: Nicotiana sylvestris (wood tobacco) (Species: Nicotiana sylvestris (wood tobacco) (Species: No. Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001 (Speciession: $4252, 1994 #sequence_revision 10-Sep-1999 #text_change 19-Jan-2001 (Speciession: M.; Sugita, M.; Sugi
                                                                                                                                                                                                                                                                                            A;Introns: 107/2; 173/2; 228/3; 594/3; 1165/2; 1216/3; 1231/3; 1258/2; 1300/2; 1321/3; 1 C;Superfamily: LDL receptor ligand-binding repeat homology <LDL>
P;11-45/Domain: LDL receptor ligand-binding repeat homology <LDL>
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A,Experimental source: strain PA01
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A; Residues: 1-607 <ITA>

A; Residues: 1-607 <ITA>

A; Residues: 1-607 <ITA>

A; Residues: 1-607 <ITA>

A; Residues: 1-607 <ITA

C; Superfamily: tobacco AIP-dependent RNA helicase DB10; WW repeat homology

C; Keywords: AIP; nucleotide binding; P-loop

P; Residues: MW repeat homology <WW1>

P; 189-196 (Region: nucleotide-binding motif A (P-loop)

P; 294-299 (Region: nucleotide-binding motif B

P; 298-301/Region: DEAD motif
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38.9%; Score 45.5; DB 1; Length 607;
Best Local Similarity 37.9%; Pred. No. 44;
Matches 11; Conservative 4; Mismatches 5; Indels
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Pred. No. 1e+02;
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C,Superfamily: Fe2+-dicitrate sensor, transmembrane component
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A,Molecule type: DNA
A,Residues: 1-1609 <AND>
A,Cross-references: EMBL:L23646; NID:g388595; PID:g388601
C;Genetics:
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Best Local Similarity 66.7%;
Matches 8; Conservative
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877 LLEGRISCVVSS 888
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A; Residues: 1-316 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: DNA
A, Residues: 1-489 <COL>
A, Cross-references: GB: Z77163; GB: AL123456; NID: G3261610; PIDN: CAB00967.1; PID: G1449352
A; Experimental source: strain H37Rv
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome
                                                       cytochrome P450 Rv2268c - Mycobacterium tuberculosis (strain H37RV)
N;Contains: oxidoreductase (EC 1.....)
C;Species: Mycobacterium tuberculosis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: H70729
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devilin, K.; Feltwell, T.; Gentles, S.; Harris, D.; Gordon, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squres, S.
Nature 393, 537-544, 1998
NAturbors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A,Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A, Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL117389; PIDN:CAB55767.1; GSPDB:GN00068; SPDB:SPCC4F11.01
A;Experimental source: strain 972h-; cosmid c4F11
C;Genetics:
A;Gene: SPCC4F11.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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S44821
14482.4 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Aug-1998
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Aug-1998
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Aug-1998
C;Anderson, K,
submitted to the EMBL Data Library, September 1993
A;Paescription: Sequence of the C. elegans cosmid F44E2.
A;Reference number: S44816
A;Accession: 944821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
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C.Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology
C;Keywords: oxidoreductase
F;322-457/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 29;
4; Mismatches 7; Indels
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39.3%; Score 46; DB
Best Local Similarity 40.9%; Pred. No. 43;
Matches 9; Conservative 5; Mismatches
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Best Local Similarity 47.6%;
Matches 10; Conservative
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RESULT 10 T41352

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Search completed: May Job time : 22 secs
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(Species: Mycobacterium tuberculosis
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A, Raference number: A70500; MUID:9829597; PMID:9634230

A, Reference number: A70500 (Mycobacterium tuberculosis from the complete genome A, Reference number: DNSO6

A, Residues: Dreliminary; nucleic acid sequence not shown; translation not shown

A, Residues: 1-512 (CDL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z98209; GB:AL123456; NID:g3261838; PIDN:CAB10909.1; PID:g2292967
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2733c
C;Superfamily: conserved hypothetical protein b0835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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                                                     195 RVAVLAGRVE--LSPLHGRGRW 214
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Matches 11; Conserv
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Gaps
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                7; Indels
Best Local Similarity 47.1%; Pred. No. 92; Matches 8; Conservative 2; Mismatches
                                                                                                                                         6, 2004, 12:47:27
                                                                        296 EGTYECEAENIKGRDTY 312
                                                   7 EGRTECVLSNLRGRTRY 23
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38.5%; Score 45; DB 2; Length 1036;

A;Cross-references: EMBL:X79607 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994 C;Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology

Superfamily: contactin; fibronectin type III repeat 1; Reywords: cell adhesion 1,1-23/Domain: signal sequence #status predicted <SIG> 1,24-1036/Product: axonin 1 #status predicted <MAT>

F;336-392/Domain: immunoglobulin homology < IMM>

Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA

NyAlternate names: neural cell adhesion molecule AxCAM
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: S22383; S34107; S69323; S22128
R;Zuellig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohlen und Halbach, F.; C
A;Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, immu A;Reference number: S22383; MUID:92174898; PMID:1311675

1 QRVEIL----EGRIECVLSNLRGRIR 22

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axonin 1 precursor - chicken

A; Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;33 R;Giger, R.J.; Vogt, L.; Zuellig, R.A.; Rader, C.; Henehan-Beatty, A.; Wolfer, D.P.; Son Biochem. 227, 617-628, 1995
A;Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter. A;Reference number: S69332; MUID:95172044; PMID:7867620

olecule type: mRNA esidues: 1-1036 <ZUE1> ross-references: EMBL:X63101; NID:g62852; PIDN:CAA44815.1; PID:g62853

Molecule type: protein

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us-10-612-885a-1.rag

1028 2 AAW29667 . Aaw29667 49 4 AAB84225 Aab8422	49 41.9 221 5 ABP65639 App65639 49 41.9 286 5 ABP43791 Abp43791 40 41.0 331 5 AVANA136	40 41.9 341 40 41.9 341 40 41.9 373	49 41.9 413 4 AAB694220 ARB032220 49 41.9 451 4 AAB66063 AB65063 49 41.9 451 6 AB032717 AB06063 49 41.9 451 6 AB032717 AB06063	49 41.9 456 6 AB032693 AD032693 SECTED 49 41.9 456 2 AB032693 AD032693 AD03	49 41.9 470 4 AAB66083 49 41.9 470 4 AAB66083 40 41 0 470 6 ARTIORYTI	11000000 11000000 0 0.15 C.15 C.	ALIGNMENTS	RESULT 1 AAY39411 D AAY39411 standard, peptide; 23 AA.	AC AAY39411;	DT 30-NOV-1999 (first entry)	XX DE Human erythropoietin receptor-derived activation peptide.	XX XW Erythropoietin, EPO, receptor, activation, internalisation.	AX OS Synthetic.	WO994	XX PD 26-AITG-1999	XX XX PF 23-FEB-1999; 99WO-US003910.	XX PR 24-PEB-1998; 98US-00028938.	XX PA (RECE-) RECEPTRON INC.	AA PI Olsson L, Naranda T;	XX DR WPI; 1999-527422/44.	PT Modulating activity of type-2 cell surface receptors used in treatment	יים ביים ביים ביים ביים ביים ביים ביים	XX XX	CC This sequence represents a peptide derived from the extracellular CC activation sequence of the human erythropoiethin (EPO) receptor.	CC are separate from the ligand binding site, Activation sequences are	CC internalisation; and/or in the modulation of activation of the receptor.	CC Use of peptides corresponding to the activation sequence of a receptor CC can retard or inhibit receptor internalisation, thereby increasing or	CC stabilising the steady-state number of active receptors on the Cell. CC surface. This has the effect of increasing signalling per unit of ligand.	CC In Addition, the receptor is transed as a type a term outside terminal of meaning that such apptides can actually replace the requirement for the	CC ligand, causing iigand-independent activation. The activation to CC probably brought about by a dimerisation mechanism in which one peptide	
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	protein search, using sw model	May 6, 2004, 12:38:56; Search time 54 Seconds (without alignments) 120.344 Million cell updates/sec	US-10-612-885A-1	BLOSUM62 Gapop 10.0 , Gapext 0.5	1586107 seqs, 282547505 residues	of hits satisfying chosen parameters: 1586107	eq length: 0	 50			3: geneseqp2000s:* 4: geneseqp2001s:*			results predicted b	by analysis of the total score distribution.	SUMMARIES	Query' ce Match Length DB ID Description	100.0 23 2 AAY39411 AAY39411	100.0 23 5 AAU/8011 AAU/8011 100.0 23 6 ABP72837 Abp72837	100.0 30 2 AAR98938 Aar98938 100.0 211 3 AAB21686 Aab21686	100.0 438 3 AAY44622	100.0 458 7 ABE28671 Ade28671 Ade28671	100.0 458 / ADE28675 . Ade28675 100.0 458 7 ADE28675 Ade28675		100.0 508 2 AAR47518 Aar47518 Aar47518	100.0 508 2 AAR70032 AAR70032 100.0 508 2 AAR69503 Aar69503	100.0 508 5 ABB09173 Abb09173 94.9 508 7 ADE28677 Ade28677	93.2 265 2 AAR50326 Aar50326 Mouse sol	93.2 507 2 AAR47517 Aar47517 MEL BPO r 93.2 507 2 AAR69502 Aar69502 Mouse ery	87.2 507 2 AAK50327 AAT50327 Mou. 44.4 1026 5 AAU80379 Aau80379 Hum	
	OM protein - p	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number o	Minimum DB seq Maximum DB seq	Post-processin	Database :					Pred. No	and is		Result No. Score							12 117							

Length 23;

Sequence 23 AA;

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This invention corresponds to a novel composition comprising any of 34 denains of cell-surface receptors. These peptides were identified by chamology searching with a peptide sequence from the MHC class I alpha I connected to the activation sequence from the MHC class I alpha I connected to the activation sequence from the internalisation of creeptor and so these peptides may be used to modulate the internalisation and or activation of these receptors. The peptides of the invention may also be used to increase effect of ligand signalling in type 2 diabetes and can replace the ligand normally required for activation. This is useful when the ligand normally required for confunction as antagonists of receptor signalling. The peptides may also interact synergistically with the ligand or function as ningand or signalling. The peptides may also interact synergistically with the ligand or function as ligand replacements. Use of these peptides can increase the effect of therapeutic hormons of the ceptor internalisation or function as ligand replacements. Use of these peptides can increase the effect of therapeutic hormons of continciants from which they derive. The present sequence represents the human the invention Erythropoletin receptor activation sequence oligopeptide of the invention
s bound by two receptors, mimicking the dimerisation and activation that occurs when two receptors bind one ligand. Is could be used to treat disorders involving an inadequate or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising peptides from receptor extracellular domains, useful for e.g. modulating receptor internalization and activation such as increasing insulin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brythropdietin receptor; antidiabetic; activation sequence; ligand; receptor internalisation; type 2 diabetes; drug screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human erythropoeitin receptor activation domain oligopeptide.
                                                                                                                                    Length 23;
                                                                                                                                  100.0%; Score 117; DB 2; Length 2
100.0%; Pred. No. 3.6e-11;
ive 0; Mismatches 0; Indels
                                                          inappropriate response from its corresponding receptor
                                                                                                                                                                                                              ORVEILEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                                                                AAU78011 standard; peptide; 23 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Col 11; 48pp; English
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97US-00788820.
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                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                Query Match Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RECE-) RECEPTRON INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Naranda T;
is bound by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-224899/28.
                                                                                                Sequence [23 AA;
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22-AUG-1996;
23-JAN-1997;
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                                      This peptide
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                  subsequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olsson L,
                                                                                                                                                                                                                                                                                                                                                                                        AAU78011
                                                                                                                                                                                                                                                                                                          RESULT 2
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                                                                                                                                                                                                                                                                                                                                                antiparkinsonian; nootropic; anti-HIV; antiasthmatic; antiallergic; cytostatic; immunosuppressive; antiatherosclerotic; cardiant; gynaecological; immunostimulant; antianaemic; haemostatic; antiinflammatory; dermatorlogical; antibacterial; virucide; antiparasitic; fungicide; hepatotropic; antirheumatic; antiarthritic; antigout; tranquillizer; vulnerary; antidiabetic; nephrotropic; antipyretic; gastrointestinal; gene therapy; transgenic animal; erythropoietin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion protein, useful in the diagnosis and treatment of diseases or disorders relating to the respiratory, cardiovascular and digestive systems, comprises a transferrin protein fused to a therapeutic protein.
                                    Gape
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                                                                                                                                                                                                                                                                                                                                     Transferrin; neuroprotective; cerebroprotective; vasotropic;
                                  Indels
Score 117; DB 5;
Pred. No. 3.6e-11;
                                  Mismatches
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                                                                                                    ORVEILEGRÍECVLSNÍRGRÍRY 23
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                                                                       1 ORVEILEGRIECVLSNLRGRIRY
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                                                                                                                                                                                                                                                                                                      Erythropoietin mimetic peptide.
                                                                                                                                                                                            ABP72837 standard; peptide; 23
 100.0%;
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                                                                                                                                                                                                                                                                   (first entry)
                                  Conservative
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 Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mimetic; agonist
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                                                                                                                                                                                                                                                                   11-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                 ABP72837;
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                                                                                                                                                         RESULT 3
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100.0%; Score 117; DB 6; Length 23;

infectious diseases, or to delacross the blood-brain barrier

Sequence 23

Query Match

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The present invention relates to a method for screening for a ligand analog, comprising adding a candidate ligand to a non-naturally occurring cell surface receptor analog e.g. erythropoietin receptor (BPOR), and determining the binding of the ligand to the analog. The present sequence is a mature human erythropoietin receptor (BPOR) extracellular domain. Protein Design Automation was carried out on the present sequence, so that it may be used in the present invention as a cell surface receptor
                                                                                                                                                                                                                                                                                                                                                                            Screening for ligand analogs and agents which modulate ligand-receptor binding, comprises adding a test ligand to a non-naturally occurring cell surface receptor analog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mature erythropoietin receptor BPOR extracellular domain #1.
Human mature erythropoietin receptor BPOR extracellular domain
                                 cell surface receptor; erythropoietin; EPOR; human; design automation; PDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ligand; cell surface receptor; erythropoietin; BPOR; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 100.0%; Score 117; DB 3; Local Similarity 100.0%; Pred. No. 4.7e-10; Nes 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORVEILEGRITECVLSNLRGRIRY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB21685 standard; peptide; 225 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QRVEILEGRTECVLSNLRGRTRY
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                                                                                                                                                                                       11-FEB-2000; 2000WO-US003665
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                                                                                                                                                                                                                                                                          (XENC-) XENCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (XENC-) XENCOR INC.
                                                                                                                                                                                                                                                                                                          Dahiyat B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 211 AA;
                                                                                                                      WO200047612-A2
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29-APR-1999;
                                                                                      Homo sapiens
                                                                                                                                                                                                                       11-FEB-1999;
                                                                                                                                                                                                                                         29-APR-1999,
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                                                        protein
                                     Ligand;
                                                                                                                                                                                                                                                                                                          Luo P,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR89960-R89965 and AAR98936-R98939 are overlapping, synthetic human erythropoletin receptor (sHuBPOR) peptides which span readdues 1 to 244 of the human BPOR. The peptides are used to map the BPOR binding epitope of an BPOR monoclonal antibody which binds to BPORs and stimulates erythropolesis by stimulating the proliferation and/or differentiation of erythrod progenitor cells to erythrocytes. Pharmaceutical compsns. contg. the antibody may be used in the diagnosis and treatment of patients having disorders associated with low red blood cell levels, e.g. anaemia. The antibodies are also useful in methods and kits for detecting BPORs in biological in biological samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibodies stimulating an erythropoietin receptor - useful in diagnosis and treatment of patients having disorders associated with low red blood cell levels, e.g. anaemia.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                            Monoclonal antibody, erythropoietin receptor; diagnosis, anaemia; erythropalesis, erythrocyte production; epitope mapping.
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                      Indels
                                                                                                                                                                                                                                                                            human erythropoietin receptor peptide, SE-8.
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100.0%; Pred. No. 4.9e-11;
iive 0; Mismatches 0;
       100.0%; Pred. No. 3.6e-11;
                      Mismatches
                                                      23
                                                                      QRVEILEGRIECVLSNLRGRIRY 23
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                                                                                                                                                                       standard; peptide; 30 AA
                                                   ORVEILEGRIECVLSNLRGRIRY
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       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1995;
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                                                                                                                                                                                                                                                                            Synthetic
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Best Local
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     Best Local
Matches '
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RESULT 5

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Indels

Length 211;

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Bell D,
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                                                                                                  The present invention relates to a method for screening for a ligand analog, comprising adding a candidate ligand to a non-naturally occurring cell surface receptor analog e.g. erythropoietin receptor (BPOR), and determining the binding of the ligand to the analog. The present sequence is a mature human erythropoietin receptor (BPOR) extracellular domain. This sequence may be used in the present invention as a cell surface
                                        for ligand analogs and agents which modulate ligand-receptor
comprises adding a test ligand to a non-naturally occurring cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serum free defined medium useful for the efficient culture of stem cells
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Truncated human EpoR, erythropoietin receptor; hypersensitive EpoR(t
mutant human EpoR; EpoR signalling; cancer; infectious disease; HIV;
sickle cell anaemia; cytostatic; antimicrobial; antiviral;
                                                                                                                                                                                                                           ö
                                                                                                                                                                                                      Score 117; DB 3; Length 225; Pred. No. 5e-10; Mismatches 0; Indels (
                                                                                                                                                                                                                                                           ORVEILEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                                                                                                                                                      AAY44622 standard, protein; 438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production of hemoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mueller SG;
                                                                                1, Fig 8, 82pp, English.
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                                                                                                                                                                                                        100.0%;
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99CA-02260332
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                human EpoR(t439)
                                                                                                                                                                                                                             Conservative
                                                              receptor analog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matthews KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-136979/12.
P-PSDB; AAZ49634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMOSOL INC
                    WPI; 2000-549135/50
                                                                                                                                                                                                    Query Match Best Local Similarity
  Dahiyat B;
                                                                                                                                                                                     Sequence 225 AA;
                                                                                                                                                                   analog
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaptene
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                                         Screening
                                                                                                                                                                                                                                                                                                                                                                                  Truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                     binding,
                                                                                                                                                                   receptor
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                                                                                  Example
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  Luo P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serum free defined medium useful for the efficient culture of stem cells
anaemia, and conditions related to abnormal expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Truncated human EpoR; erythropoietin receptor; hypersensitive EpoR(t mutant human EpoR; EpoR signalling; cancer; infectious disease; HIV; sickle cell anaemia; cytostatic; antimicrobial; antiviral; immunostimulant; anti-anaemic.
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                                                                                                            Length 438;
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                                                                                                              Score 117; DB 3;
Pred. No. 1.1e-09;
                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                    QRVBILEGRIECVLSNLRGRIRY 216
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                                                                                                                                                                                                       1 QRVEILEGRIECVLSNLRGRIRY
                                                                                                                                                                                                                                                                                                                                                                   AAY44623 standard; protein; 438
                                                                                                                100.0%;
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                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                              Query Match
Best Local Similarity
HIV), sickle cell
of erythropoietin
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                                                                      Sequence 438 AA;
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25-JAN-1999;
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RESULT 9 ADE2867

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ADE28671

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Claim 1; SEQ ID NO 48; 447pp; English.
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Matches 23; Conservative
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17-DEC-2001;
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Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N
                                                                                                                                                                                                                                                                                                          NOVX; antidiabetic; anorectic; cardiant; hypotensive; antidiabetic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiparmatory; dermatological; antiarthratic; antialpaemic; metabolic; diabetes; obseity; infectious; anorexia; cancer; cardiovascular; hypertension; atherosclerosis; neurodegenerative; Alzeimer's disease; Parkinson's; epilepsy; immune; osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia; neurogensisis; call differentiation; proliferation; haemopoiesis; wound healing; anglogenesis; gene therapy; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated NOVX polypeptides and polynuclectides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
QRVEILEGRTECVLSNLRGRTRY 216
                                                                                                                    ADE28671 standard; protein; 458 AA
                                                                                                                                                                                                                                                                 Human NOV15a protein - SEQ ID 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001; 2001US-0338628P.
05-DEC-2001; 2001US-0338660P.
07-DEC-2001; 2001US-033828FP.
12-DEC-2001; 2001US-0341346P.
17-DEC-2001; 2001US-0341540P.
20-DEC-2001; 2001US-0341540P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2001; 2001US-0344297P.
31-DEC-2001; 2001US-0344903P.
17-APR-2002; 2002US-0373288P.
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28-MAY-2002; 2002US-0383744P.
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07-AUG-2002; 2002US-0401788P.
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N-PSDB; ADE28670.
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(CURA-)

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The invention relates to a novel isolated NOVX polypeptide. The cardiant cardiant of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiatteriosclerotic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antiathmaterial, cardianteside, noteropethic, antiathritic, antiathmatory, antiathritic, antiathmatory, antiathmatic and antilipaemic activities. The colypeptides, nucleic acid molecules and antibodies may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer, cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertension and dyslipidaemia.

Cardiovascular diseases including hypertension and atherosclerosis, cardiovascular diseases including hypertensis and disease, parkinson's disease, inflammatory skin disorders as them and dyslipidaemia.

Cut disorders, inflammatory skin disorders as thima and dyslipidaemia.

Cut disorders, inflammatory skin disorders, asthma and dyslipidaemia.

Cut disorders, inflammatory skin disorders, asthma and dyslipidaemia.

Cut disorders as well as in gene therapy. Finally, the nucleic acide may be used as hybridisation probes, in chromosome mapphing, tissue typing, be used as hybridisation probes, in chromosome mapphing, tissue typing, be the human NOV protein of the invention:
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100.0%; Pred. No. 1.1e-09;
tive 0; Mismatches 0;
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ID ADE28673 standard; protein; 458 AA.
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, 2001US-0342592P.
, 2001US-0344297P.
, 2001US-0344903P.
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31-DEC-2001;

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antidiabetic; anorectic; cardiant; hypotensive;
Human NOV15c protein - SEQ ID 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alsobrook JP, Alvarez B, Anderson DW, Baron M, Boldog FL;
Burgess CE, Caeman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K;
Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M;
Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
Smithson G, Starling G, Spyrek KA, Stone DJ, Tchernev VT, Twomlow N;
Vernet CAM, Zerhusen BD, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiarterioscierotic, virucide, anorectic, funcide, protozoacide, nocuropic, eneroprotective, antiparkinsonian, anticonvulsant, osteopathic, antiarthritic, antiinflammatory, actionovalsant, osteopathic, antiarthritic, antiinflammatory, polypeptides, nucleic acid molecules and antibodies may be useful for treating or diagnosing diseases including metabolic disorders such as disbetes and obesity, infectious diseases, anorexia, cancer, cardiovascular disorders sincluding hypertension and atherosciarosis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders as a sthma and dyshipidemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
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                                                                                                                                                         2002US-0383744P.
2002US-0383829P.
2002US-0384024P.
2002US-0401788P.
2002US-0406553P.
                                                                          2002US-0381495P.
                                           2002US-0380981P
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23; Conservative
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N-PSDB; ADE28672.
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                                   15-MAY-2002; 2
17-MAY-2002; 2
28-MAY-2002; 2
                                                                                                                                                             28-MAY-2002;
29-MAY-2002;
29-MAY-2002;
07-AUG-2002;
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31-OCT-2002;
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Best Local
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Alsobrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL; Burgess CE, Caman SJ, Chapoval A, Dhanbal M, Edinger SR, Eisen A; Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L; Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV; Lepley DM, Li L, Macdougall JR, Malyankar UM, Mazur A, Mcqueeney K; Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patturajan M; Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA; Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N Vernet CAM, Zerhusen BD, Zhong M;
                                            antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic; antiinflammatory; dermatological; antiarthritic; antilifammatory; dermatological; antiarthritic; antilipaemic; metabolic; diabetes; obesity; infectious; ancexta; cancer; cardiovascular; hypertension; atherosclerosis; neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune; osteoarthritis; hemopoletic; inflammatory skin; asthma; dyslipidaemia; neurogenesis; cell differentiation; proliferation; haemopolesis; wound healing; anglogenesis; gene therapy; chromosome mapping; tissue typing; human; NOV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel isolated NOVX polypeptide. The polypeptide of the invention demonstrates, antidiabetic, anorectic, cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial, fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian, anticorvulaant, osteopathic, antiarthritic, antiinflammatory, dermatclogical, antiathmatic and antilipaemic activities. The polypeptides, nucleic acid molecules and antibodies may be useful for treating or diagnosing diseases including metabolic disorders such as diabetes and obesity, infectious diseases, anorexia, cancer,
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2001US-0341346P.
2001US-0341477P.
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2001US-0342592P.
2001US-0344297P.
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2002US-0381495P
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2002US-0383744P
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27-DEC-2001;
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15-MAY-2002;
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Gaps

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Indels

0; Mismatches

Matches

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23

194 QRVEILEGRIECVLSNLRGRIRY 216

QRVEILEGRTECVLSNLRGRTRY

ADE28675 standard; protein; 458 AA.

RESULT 11 ADE28675

(first entry)

29-JAN-2004

ADE28675

XXXEX

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Indels

us-10-612-885a-1.rag

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Purthermore, the nucleic acids and polypeptides may also be used to identify molecules that modulate or inhibit neurogenesis, cell afferentiation and proliferation, haemopolesis, wound healing and angiogenesis, as well as in gene therapy. Finally, the nucleic acids may be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The current sequence is that of
cardiovascular diseases including hypertension and atherosclerosis, envodespenzative disorders such as Alzheimer's disease, Parkhinson's disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic disorders, inflammatory skin disorders, asthma and dyslipidaemia.
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251. .254
/note= "Pactor Xa cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 117; DB 7; Length 458; 100.0%; Pred. No. 1.1e-09;
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/label= Fc
/note= "human IgG1 Fc sequence"
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                                                                                                                                                                                                                                                                               the human NOV protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRVEILEGRIECVLSNLRGRIRY 23
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/label= EpoR-ECD
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Matches 23; Conserv
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N-PSDB; A
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Chimeric.
                                                                                                                                                                                                                                                                                                                                             Sequence
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Domain
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fused (via a Factor Xa cleavage sequence) to the Fc portion of human IgG1. It can be expressed e.g. in transfected Drosophila 52 cells upon induction with copper sulphate. The cells secrete BpoRFc as a dimeric molecule due to the affinity of the Fc moiety for itself. The dimeric receptor can be used as an immunogen to generate antibodies (monoclonal, polyclonal, chimeric, humanised) able to act as BcoR agonists for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Site specific label; detection; interaction screening; transglutaminase; erythropoietin receptor; BPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to methods for the site specific modification of protein, and to a method for screening for a candidate compound which interacts with first protein. The screening method comprises contacting the candidate molecule with a labelled modified first protein and detecting the label to identify interaction of the labelled modified first protein and candidate compound. The first protein is modified to contain a peptide, represented by sequence AAB13005. The method is used to label proteins at specific sites. The present sequence represents a Q tagged erythropotetin (BPO) receptor constructed in an example of the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for a candidate compound for use in bioassays comprises contacting the candidate molecule with a labelled modified protein and detecting the label to identify interaction of the two molecules.
                                                                                                                                                                                                              Gaps
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Pred. No. 1.2e-09;
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100.0%; Pred. No. 1.3e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2-tagged erythropoletin (BPO) receptor protein.
                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                     194 QRVEILEGRIECVLSNLRGRIRY 216
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                                                                                                                                                                                                                                                                                                                                                                     AAB13012 standard; protein; 503
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                                                                                                                                                                            100.0%;
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                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 23, Conservative
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18s 23; Conservative
                                                                                       polyclonal, chimeric
treatment of anaemia
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                                                                                                                                         Sequence 488 AA;
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comprises

A fusion

/note= "putative transmembrane domain"

/note= "mature BPO receptor" 251. .272

1. .24 /note= "signal peptide"

.508

Protein Peptide

Region

Location/Qualifiers

Homo sapiens

Key

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The sequence was deduced from DNA obtd. from a clone isolated from a commercially available human geenomic cDNA library in phage Lambda Fix (Stratagene). The sequence encodes a type I trans- membrane protein with binding Affinity for EDO. The gene and recombinant EPO receptor produced on expression of the DNA are used to develop reagents and systems to control and study erythropoiesis. It is believed that the EPO receptor is dys- functional in individuals with Diamond Blackfan anaemia, and may be hyperactive in polycythemia vera. See also ARN0511 (murine EPO receptor), (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erythropoletin receptor and gene - used for developing reagents and systems to control and study erythropolesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 508;
                                                                                                                                                                                                         Erythropþietín; Diamond Blackfan anaemia; polycythemia vera.
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Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
(WHED ) WHITEHEAD INST BIOMEDICAL RES.
194 QRVEILEGRIECVLSNLRGRIRY 216
                                                                          AAR06512 standard; protein; 508 AA.
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                                                                                                                                                                                                                                                                                                                               89US-00306503
                                                                                                                                                                                                                                                                                                                                                           89US-00306503
                                                                                                                                  (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Wong G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ05748
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                                                                                                                                                                                                                                           Homo saptens.
                                                                                                                                                                               EPO receptor
                                                                                                                                                                                                                                                                                                                               03-FEB-1989;
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04-JAN-1991
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                                                                                                       AAR06512
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                                            RESULT 14
                                                          AAR06512
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prods.

Recombinant DNA encoding erythropoietin receptor - used to develop for study, treatment or diagnosis of disorders in which receptor is dysfunctional.

Disclosure; Fig 9; 24pp; English.

(CHIL-) CHILDRENS MEDICAL CENT. (WHED) WHITEHEAD INST BIOMEDICAL RES

(GEMY) GENETICS INST INC.

91US-00678877. 89US-00306503

25-MAR-1991;

11-JAN-1994. US5278065-A.

03-FEB-1989;

D'andrea A, Wong GG, Jones SS

WPI; 1994-025409/03. N-PSDB; AAQ53995.

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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse erythroleukaemia (MEL) cells were used to construct a cDNA library. The cDNA was used to transfect COS-1 cells and these were screened for radiolodinated erythropoietin (BPO) binding to isolate cDNA encoding the BPO receptor. This cDNA was used as a probe to screen a human genomic cDNA library to obtain DNA was used as a probe to screen a human genomic cDNA library to obtain DNA encoding the human EPO receptor. The CDNA may be used to study, treat or diagnose disorders in which the BPO receptor is dysfunctional. The EPO receptor may also be used to raise antibodied or The pord. Is pref. used for treating anaemias, primary proliferative polycythemia and secondary polycythemia. See also AAR47517. (Updated on 25-MAR-2003 to correct PF field.)
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6, 2004, 12:45:02

Search completed: May Job time : 55 secs

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ORVEILEGRIECVLSNLRGRIRY 216

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AAR47518 standard; protein; 508 AA.

RESULT 15 AAR47518

ORVEILEGRIECVLSNLRGRIRY 23

Erythrophietin receptor; recombinant; murine; anaemia.

(first entry)

Human EPO receptor.

(revised)

25-MAR-2003 24-JUN-1994

ZXZXEEXEXEX Z

AAR47518

42 35.9 4472 2 US-08-804-227C-2 Sequence 42 35.9 4545 2 US-08-804-227C-14 Sequence 41 35.0 50 4 US-09-621-976-6312 Sequence 41 35.0 60 4 US-08-754-477A-14 Sequence	32 41 35.0 60 4 US-08-754-477A-15 Sequence 15, Appl 33 41 35.0 75 3 US-09-73818-13 Sequence 13, Appl 34 41 35.0 292 4 US-09-711-164-438 Sequence 438, App 35 41 35.0 292 4 US-09-713-001C-3535 Sequence 3535, Ap 36 41 35.0 749 4 US-09-134-001C-3535 Sequence 17331, App 4 US-09-758-291A-17331 Sequence 17331, App 4 US-09-758-281B-155 Sequence 155, App	41 35.0 835 4 US-09-758-282B-243 Sequence 41 35.0 843 4 US-09-489-039A-545 Sequence 41 35.0 865 4 US-09-252-991A-20894 Sequence 41 35.0 1018 1 US-08-408-093-6 Sequence	41 35.0 1018 1 US-08-408-420A-6 Sequence 41 35.0 1018 1 US-08-714-901-6 Sequence 41 35.0 1018 3 US-08-040-741-6 Sequence 41 35.0 1019 3 US-08-040-741-6 Sequence	SENERAL COST OF TARREST OF TARRES		US-09-028-937-11 ; Sequence 11, Application US/09028937 ; Patent No. 6333031 ; GENERAL INFORMATION:	APPLICANT: Olsson, Lennart APPLICANT: Naranda, Tatjan TILLE OF INVENTION: Receptor Derived Peptides As Modulators TILLE OF INVENTION: Of Receptor Activity NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS: ADDRESSER: Flehr, Hobbach, Test, Albritton & Herbert STREET: 4 Embarcadero Center, Suite 3400	CUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: 04111-4187	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk : COMPUTER: TRM PC COMPATIALE) OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	CORRELATION DAIA: APPLICATION NUMBER: US/09/028,937 FILING DATE: CLASSIFICATION:	; PRIOR APPLICATION NUMBER: US 08/788,820 ; FILING DATE: 23-JAN-1997	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/701,382 ; FILING DATE: 22-AUG-1996	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/612,999 ; FILING DATE: 08-MRR-1996	HIGHER STANDIN INCOMMILION: NAME: SILVA, RODIN M. REGISTRATION NUMBER: 38,304 REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS	TELEPHONE: (415) 781-1989 TELEPHONE: (415) 781-1989 TELEPHONE: (415) 784-8711	INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: 	1 ITE: maino acia ; STRANDEDINESS: unknown ; TOPOLOGY: unknown ; MOLECULE TYPE: protein US-09-028-937-11
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model Run on: May 6, 2004, 12:42:22 ; Search time 23 Seconds (without alignments) 51.626 Million cell updates/sec	Title: US-10-612-885A-1 Perfect score: 117 Sequence: 1 QRVEILEGRIECVLSNLRGRIRY 23	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 389414 seqs, 51625971 residues Total number of hits satisfying chosen parameters: 389414	um DB seg length: 0 um DB seg length: 2000000000	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries	Database: Issued_Patents_AA:* 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:* 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 6: /cgn2_6/ptodata/2/iaa/BaCMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	117 100.0 23 4 US-09-028-937-11 117 100.0 30 2 US-08-280-864A-12 117 100.0 30 4 US-09-092-291-12	11/ 100.0 438 4 US-09-359-838-5 Sequence 11/ 100.0 488 3 US-08-776-511-2 Sequence	11/ 100.0 508 2 US-08-850-293-5 Sequence 49 41.9 321 3 US-09-039-609-4 Sequence 49 41.9 458 3 US-09-039-609-2 Sequence	46 39.3 64 4 US-09-134-000C-5287 Sequence 45 39.3 67 4 US-09-732-210-1599 Sequence 45 39.3 67 4 US-09-732-210-1600 Sequence 75 77 116-09-73-210-1600 Sequence	4 37.6 493 4 US-09-489-0394-12903 Sequence 43 36.8 931 4 US-08-624-655A-2 Sequence 42 35.9 67 4 US-09-732-210-1601 Sequence	42 35.9 252 4 US-09-252-991A-32222 Sequence 42 35.9 283 4 US-08-956-171E-5203 Sequence 42 35.9 363 4 US-08-914-000C-3764 Sequence 43 35.9 363 4 US-08-373-000C-3764 Sequence	42 35.9 605 2 05-08-10-5-30.8-8 Sequence 42 35.9 605 4 08-09-701-802-8 Sequence 42 35.9 605 4 08-09-911-326-8 Sequence 45 35.9 605 4 103-09-911-326-8 Sequence	24 42 35.9 1018 1 US-08-452-0522 Sequence 2.330, A 25.9 1018 1 US-08-465-052 Sequence 2. Appli 25 42 35.9 1101 3 US-08-966-485-2 Sequence 2. Appli 26 42 35.9 1611 2 US-08-964-227C-5 Sequence 5. Appli 27.9 35.9 3729 2 US-08-804-227C-4 Sequence 4, Appli

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Best Local Similarity 100.0%; Score 117; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,291
                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 117; DB 4; 100.0%; Pred. No. 1.8e-12;
                                                                                     PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 25-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B:
REPRENCE/DOCKET NUMBER: A-307A
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 QRVEILEGRIECVLSNLRGRIRY 216
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Patent No. 6361998
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bell, David N. APPLICANT: Mueller, Susan G.
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-09-092-291-12
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US-09-339-838-5
                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-339-838-5
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US-09-339-838-7
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             Length 23;
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                                                Indels
                                                                                                                                                                                          Sequence 12, Application US/08280864A
; Patent No. 5885574
; GENERAL INFORMATION:
APPLICAMT: Elliott, Steven G.
TITLE OF INVENTION: Antibodies Which Activate an TITLE OF INVENTION: Erythorpoietin Receptor
NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESPEN AMORE INC.
; STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                     STATE: CALIFORNIA CONTRACTOR CALIFORNIA COUNTRY: U.S.A.

* ZIP. 91320
COMPUTER READABLE FORM: READABLE FORM: COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/280,864A
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Elliott, Steven G.
TITLE OF INVENTION: Antibodies Which Activate an
TITLE OF INVENTION: Erythorpoietin Receptor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                 Score 117; DB 4;
Pred. No. 1.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 117; DB 2;
Pred. No. 1.8e-12;
100.0%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                    ORVEILEGRIECVLSNIRGRIRY 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09092291
Patent No. 6319499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 23; Conservative 0
                                                  23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 91320
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                        Thousand Oaks
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                 Query Match
Best Local Similarity
Matches 23; Conserv
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STREET: On
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STATE: Ca
COUNTRY:
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194 QRVEILEGRTECVLSNLRGRTRY 216
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Best Local Similarity 100.º
Matches 23, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                       STATE: MCCOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-850-293-5
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TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemogld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Sequence 2, Application US/08776511

Sequence 2, Application US/08776511

Sequence 2, Application US/08776511

SEQUENCE 6. 6139190

GENERAL INPORMATION:
APPLICANT: Brickson-Miller, Connie
TITLE OF INVENTION: Method for Obtaining Receptor Agonist
TITLE OF INVENTION: Antibodies
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKilne Beecham Corporation- Corporate
ADDRESSEE: Patents
STERFT: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                       Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:

COMPUTER:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER:

COMPUTER: IBM FC compatible

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,511

FILING DATE:

CLASSIP CATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Jervis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: 31,171

REFERENCE/DOCKET NUMBER: 31,171

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHÖNE: -10-710-5090
                                                                                                                                                                                                                                                                                                                                                       Score 117; DB 4;
Pred. No. 4.3e-11;
; Mismatches 0;
           FILE REPERBNUE: 6704-83
CURRENT APPLICATION NUMBER: US/09/339,838
CURRENT FILING DATE: 1999-06-25
FRIOR PILING DATE: 1999-01-25
FRIOR PELING DATE: 1999-01-25
FRIOR PILING DATE: 1996-01-25
FRIOR PILING DATE: 1996-06-25
NUMBER OF SEQ ID NOS: 11
SOPTWARE: Patentin version 3.1
LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 ORVEILEGRIECVLSNLRGRIRY 216
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ORVEILEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; P
Matches 23; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 488 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAK: 610-270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      King of Prussia
Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-776-511-2
                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                             US-09-339-838<mark>-</mark>7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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GENERAL INFORMATION:

APPLICANT: Lee, Jong Y.

TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 74ah & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ALBONE, EARL
APPLICANT: ALBONE, EARL
APPLICANT: ALBONE, EARL
TITLE OF INVENTION: HTHBZ47
TITLE OF INVENTION: HTHBZ47
NUMBER OF EQUENCES: 4
CORRESPONDENCES ADDRESS:
ADDRESSED: Rather & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NAME: US/08/850,293
FILING DATE: 05-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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100.0%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION 1939
PRIOR APPLICATION DATA
PPLICATION NUMBER: 08/499,643
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,815
PILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: BILINGER: MARK 8.
REGISTRATION NUMBER: 34,812
REFERENCE ADOCKET NUMBER: 07004/00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ORVEILEGRIECVLSNLRGRIRY 23
US-08-850-293-5; Sequence 5, Application US/08850293; Patent No. 5843726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/09039609; Patent No. 6107473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEBRAX: 612/286-yeyc
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 508 amino acids
TYPE: amino acids
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ORVEILEGRIECVISNIRGRIRY 23

us-10-612-885a-1.rai

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Sequence 5287, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1999-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1
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APPLICANT: Mittanck Cindy A.
APPLICANT: Mittanck Cindy A.
APPLICANT: Mittanck Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Younde S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REPERENCE: 18-21[15036]B
CURRENT APPLICATION NUMBER: US/09/732,210
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR PILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR APPLICATION NUMBER: US 60/169,340
NUMBER OF SEQ ID NOS: 1753
SEQ ID NOS: 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
41.9%; Score 49; DB 3; Length 458;
Best Local Similarity 50.0%; Pred. No. 6.3;
Matches 10; Conservative 4; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 VELLDGYTHRVLARFHGRSR 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VEILEGRIECVLSNLRGRIR 22
TELECOMMONICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VELIEGRIEEQLINM 25
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                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 458 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 60.vv
France 9; Conservative
                                                                                                                                                                                                                                                                                                                     the TOPOLOGY: linear to
                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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LENGTH: 64
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Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALBONE, EARL
APPLICANT: ALBONE, EARL
TITLE OF INVENTION: HITHBA?
NUMBER OF SEQUENCES:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE:
COUNTRY: USA
                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOCIETATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,609
FILING DATE: 16-MAR-1998
CLASSIFICATION NUMBER: 60/060,623
FILING DATE: 01-0CT-1997
APPLICATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
TELEPRAIS 610-407-0701
TELEPRAIS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZOUNTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: ISAN Compatible
CORRATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,609
FILING DATE: 16-MAR-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/060,623
FILING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Preseta, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: 23,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANBENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0%;
Matches 10; Conservative
                                 ZIP: 19482
COMPUTER READABLE FORM:
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Patent No.
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GENERAL INFORMATION:

APPLICANT:

APPLICANT:

Gary Brecon et. al

APPLICANT:

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OP INVENTION:

PIER REPERRUCE:

Z109.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE:

PRIOR PILING DATE:

1999-01-27

PRIOR PILING DATE:

1999-01-29

NUMBER OF SEQ ID NOS:

14342

SEQ ID NO 12903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAMSFERRIN-BINDING PROTEIN 1 (TDD1) GENE OF ACTINOBACILIUS DIEUCOPREUMONIAS, ITS USB TO IPRODUCTS FOR THE UTILIZATION IN VACCINES FOR PLEUROPNEUMONIA AND AS DIAGNOSTIC REAGENTS
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37.6%; Score 44; DB 4; Length 493;
Best Local Similarity 45.0%; Pred. No. 45;
Matches 9; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 931,
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33.3%; Pred. No. 1.4e+02;
tive 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/624,655A
CURRENT FILING DATE: 1996-03-22
PRIOR APPLICATION NUMBER: 95 00592
PRIOR FILING DATE: 1995-03-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 931
TYPE: PRT
ORGANISM: Actinobacillus pleuropneumoniae
                                                                                                                                                          Sequence 12903, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 6, 2004, 12:46:53
Job time : 23 secs
                                           251 RVAVLAGRVE--LSPLHGRGRW 270
  2 RVBILEGRTECVLSNLRGRTRY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08624655A Patent No. 6323005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 EALEGKTPCVRVKRRGKHEF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 EILEGRIECVLSNLRGRIRY 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DABAN, MONTSERRAT
APPLICANT: MEDRANO, ANDRES
APPLICANT: ESPUNA, ENLIC
APPLICANT: OURROL, ENRIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 33.5.5
Best Local Similarity
6, Conservative
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: P007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                              RESULT 14
US-09-489-039A-12903
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Requence 12067, Application US/09252991A

Patent No. 651705

GENERAL INPERMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
APPLICANTON: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-18
PRIOR PILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Sequence 160. Application US/09732210

Sequence 160. Application US/09732210

SENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Wu, Younie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REPREBUCE: 38-21 (15.036) B.
CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO 1600

LENGTH: 67
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54.5%; Pred. No. 22;
ive 2; Mismatches 6; Indels
                                                                                         Query Match 39.3%; Score 46; DB 4; Length 67; Best Local Similarity 42.9%; Pred. No. 2; Matches 9; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 67;
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Pred. No.
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RVEFLEDTTRTIVRNVKGPVR 49
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RVEFLEDTTRTIVRNVKGPVR 49
                                                                                                                                                                                    RVEILEGRTECVLSNLRGRTR 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONGANISM: Kluyveromyces marxianus US-09-732-210-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32067
; TYPE: PRT
; ORGANISM: Kluyveromyces lactis
US-09-732-210+1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.3%;
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Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-252-991A-32067
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US-09-732-210-1600
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ORGANISM:
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Sequence 5, Appl Sequence 16, Appl Sequence 43, Appl Sequence 373, App Sequence 3, Appl Sequence 286, Ap Sequence 5282, Ap Sequence 5282, Ap Sequence 9725, Ap Sequence 12900, A Sequence 181458, Sequence 181458,

4 US-10-029-386-27439 US-09-848-288-4 US-09-788-4 US-10-042-431-6 US-09-728-912-2 US-09-759-130B-413 US-10-042-431-8 US-10-029-386-32900 US-10-029-386-32800 US-10-029-386-328-8 US-10-029-386-328-8 US-10-029-386-328-8 US-10-162-335-48 US-10-162-335-48 US-10-162-335-48 US-10-162-335-48 US-10-162-335-48 US-10-162-335-48 US-10-162-335-8 US-10-162-335-8 US-10-162-335-8 US-10-162-335-8 US-10-162-335-8 US-10-162-335-8 US-10-162-335-8 US-10-162-335-8 US-10-162-335-8

Sequence 72012, A Sequence 46, Appl Sequence 48, Appl Sequence 50, Appl

Sequence 52, Appl Sequence 42, Appl Sequence 196518,

Sequence 236053, Sequence 65968,

ALIGNMENTS

Gaps

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Length 23; Indele

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Sequence 11, Application US/09991548.

Sequence 11, Application US/09991548.

Patent No. US20020166013A1

GENERAL INFORMATION:

APPLICANT: OLSSON, Lennart

APPLICANT: OLSSON, Lennart

APPLICANT: OLSSON, Lennart

TITLE OF INVENTION: RECEPTOR ACTIVITY

TITLE OF INVENTION: OF RECEPTOR ACTIVITY

TITLE OF INVENTION: OPTE: 21954-000-11-20

PRIOR APPLICATION NUMBER: 09/09,937

PRIOR FILING DATE: 1996-02-24

PRIOR PILING DATE: 1996-01-23

PRIOR PLILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 23
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100.0%; Score 117; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: human erythropoietin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRVBILEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   JS-09-991-548-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-991-548-11
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Sequence 12, Appl
Sequence 12, Appl
Sequence 50, Appl
Sequence 5, Appl
Sequence 142, Appl
Sequence 144, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
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Sequence 7, Appli
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                                                                                                                                             (without alignments)
152.001 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                                                                                                                          6, 2004, 12:45:07 ; Search time 42 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-287-971-48
US-10-287-971-50
US-10-287-971-52
US-09-016-159-5
US-10-287-971-54
US-10-316-194-144
US-10-316-194-144
US-10-316-194-144
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US-09-947-063-11
US-09-728-912-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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length: 2000000000
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117
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Match Length DB
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Maximum DB seg
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Fri May

us-10-612-885a-1.rapb

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GENERAL INFORMATION,

APPLICANT: Alsobrook, et al

APPLICANT: Alsobrook, et al

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHON
FILE REFERENCE: 12402-480A

CURRENT APPLICATION NUMBER: US/10/287,971

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: 60/338,626

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR FILING DATE: 2001-11-05

PRIOR FILING DATE: 2001-11-06

PRIOR FILING DATE: 2001-11-06

PRIOR FILING DATE: 2001-11-06

PRIOR PLING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: 60/333,072

PRIOR APPLICATION NUMBER: 60/333,072

PRIOR APPLICATION NUMBER: 60/333,262

PRIOR APPLICATION NUMBER: 60/393,262

PRIOR APPLICATION NUMBER: 60/393,262

PRIOR PILING DATE: 2002-07-02

PRIOR FILING DATE: 2002-07-02

PRIOR FILING DATE: 2002-08-26

NUMBER OF SEQ ID NOS: 397

SOFTWARE: CLEASEQLIST VEFSION 0.1

SOFTWARE: CLEASEQLIST VEFSION 0.1

SEGNEWARE: CLEASEQLIST VEFSION 0.1
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US-10-287-971-50

Sequence 50, Application US/10287971

PUBLICATION NO. US20040067882A1

APPLICANT: Alsobrook, et al

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHON

PILE REFERENCE: 21402-480A

CURRENT FILING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: 09/997,425

PRIOR FILING DATE: 2001-11-29

PRIOR FILING DATE: 2001-11-05

PRIOR PLICATION NUMBER: 60/338,626

PRIOR FILING DATE: 2001-11-05

PRIOR PLICATION NUMBER: 60/401,479

PRIOR PLICATION NUMBER: 60/338,026

PRIOR PLICATION NUMBER: 60/348,283

PRIOR PLICATION NUMBER: 60/348,283

PRIOR PLICATION NUMBER: 60/348,283

PRIOR FILING DATE: 2001-11-06

PRIOR FILING DATE: 2001-11-06

PRIOR FILING DATE: 2001-11-06

PRIOR FILING DATE: 2001-01-02

PRIOR FILING DATE: 2001-01-06

PRIOR FILING DATE: 2
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Best Local Similarity 100.0%; Pred. No. 5
Matches 23; Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-287-971-48
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APPLICANT: Elliott, Steven G
TITLE OF INVENTION:
FILE REFERENCE: 06843-0030-04000
CURRENT APPLICATION NUMBER: US/10/364,276
CURRENT APPLICATION NUMBER: US/10/364,276
CURRENT PILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-07-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: BPO mimetic; OTHER INFORMATION: peptide
US-10-231-494+30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-364-276+12
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           Sequence 30, Application US/10231494

Publication No. US20040023334A1

GENERAL INFORMATION:

APPLICANT: Prior, Christopher P.

TITLE OF INVENTION: Modified Transferrin Fusion Proteins
PILE REFERENCE: 54710-5001-US

CURRENT APPLICATION NUMBER: US/10/231,494

CURRENT FILING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: US 60/315,745

PRIOR APPLICATION NUMBER: US 60/334,059

PRIOR PELING DATE: 2001-11-30

NUMBER OF EEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 117; DB 16;
ilarity 100.0%; Pred. No. 1.8e-11;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Seguence
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Length 458;

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JARRALI LINGUALIA ALGOBROOK, et al TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHC FILLE OF INVENTION NUMBER: US/10/287,971

CURRENT APPLICATION NUMBER: US/997,425

PRIOR FILLING DATE: 2001-11-29

PRIOR FILLING DATE: 2001-12-29

PRIOR FILLING DATE: 2001-10-65

PRIOR APPLICATION NUMBER: 60/438,626

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR PILLING DATE: 2001-11-05

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR APPLICATION NUMBER: 60/401,679

PRIOR APPLICATION NUMBER: 60/401,679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                        APPLICATION NUMBER: US/09/016,159
FILING DATE: 30-JAN-1998
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/876,227
FILING DATE: 16-UIN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/734,097
FILING DATE: 21-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/60,525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/348,283
PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/406,181
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/393,262
                                                                                                                                                                                                                                                                                             FILING DATE: 02-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 0700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/335-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 508 amino aci
amino acid
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US-10-287-971-54
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Best Local Similarity
Matches 23; Conserv
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SEQ ID NO 54
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                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REPERENCE: 2406-2480A

THIE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REPERENCE: 2460-2480A

CURRENT APPLICATION NUMBER: US/10/287,971

PRIOR FILING DATE: 2001-11-29

PRIOR FILING DATE: 2001-10-22

PRIOR PILING DATE: 2001-10-6

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR APPLICATION NUMBER: 60/401,479

PRIOR APPLICATION NUMBER: 60/333,072

PRIOR PILING DATE: 2001-11-06

PRIOR PILING DATE: 2001-11-06

PRIOR PILING DATE: 2001-11-06
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TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Alchardson P.C., P.A.
STREET; 60 South Sixth Street, Suite 3300
                                                                                            Gaps
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1: 60 South Sixth Street, Suite 3300
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 117; 100.0%; Pred. No. 5
                                                                                                                                                                                      194 ORVEILEGRIECVLSNLRGRIRY 216
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DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATION NUMBER: 60/393,262
                                                                                                                                                                                                                                                                                                    Sequence 52, Application US/10287971 Publication No. US20040067882A1 GENERAL: INFORMATION:
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JS20020031806A1
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                                              100.0%;

    Floppy disk
    IBM compatible

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                                                                                            Conservative
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MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 23; Conserv
                                                                    Similarity
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US-10-287-971 50
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                                           Query Match
Best Local S
Matches 23
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STATE:
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US-10-287-971
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| Sequence 144, Application US/10316194
| Sequence 144, Application No. US20030215914A1
| Publication No. US20030215914A1
| GENERAL INFORMATION:
| APPLICANT: Houtzager, Erwin
| APPLICANT: Houtzager, Erwin
| APPLICANT: Sijmons, Peter C.
| TITLE OF INVENTION: A structure for presenting desired peptide sequences
| FILE REFERENCE: 2183-5610US
| CURRENT APPLICATION NUMBER: US/10/316,194
| CURRENT FILING DATE: 2002-12-10
| PRIOR APPLICATION NUMBER: US 10/016,516
| PRIOR APPLICATION NUMBER: US 10/016,516
| NUMBER OF EEC ID NOS: 173
| SOFTWARE: Patentin Ver. 2.1
| SEC ID NO 144
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                                                                                                                                                                                                                                                                     APPLICANT: Houtzager, Erwin
APPLICANT: Vijn, Irma M.C.
APPLICANT: Sijnons, Peter C.
TITLE OF INVENTION: A structure for presenting desired peptide sequences
FILE REFERENCE: 2183-5610US
CURRENT APPLICATION NUMBER: US/10/316,194
CURRENT PILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 10/016,516
PRIOR APPLICATION NUMBER: US 10/016,516
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 142
                        Gaps
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OTHER INFORMATION: Description of Artificial Sequence: IMABIS027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: IMABIS020
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Pred. No. 1.8e-08;
0; Mismatches 2; Indels (
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                      0, Indela
similarity 95.7%; Pred. No. 2.7e-09; 22; Conservative 1; Mismatches 0
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Pred. No. 2.3e-07;
                                                                                        46 ORVEINMGRIECVLSNIRGRIRY 68
                                                                 QRVEILEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRIRY 23
                                                                                                                                                                                                               Sequence 142, Application US/10316194 Publication No. US20030215914A1 GENERAL INFORMATION:
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Best Local Similarity 91.3%;
Matches 2‡; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT | ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT | ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: SITE
; LOCATION: (1)..(109)
US-10-316-194+142
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Best Local Similarity
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  Best Local
Matches 2
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Sequence 43, Application US/10316194
Sequence 43, Application No. US20030215914A1
Sequence 43, Application No. US20030215914A1
GENERAL INFORMATION:
APPLICANT: Houtzager, Erwin
TITLE NOF INVENTION: A structure for presenting desired peptide sequences
TITLE REFERENCE: 2183-5610US
CURRENT APPLICATION NUMBER: US/10/316,194
CURRENT FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
NUMBER: PSEQ ID NOS: 173
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 43
LEMOTH: 109
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                                                                                                                                                                                                                                      APPLICANT: Houtzager, Erwin
APPLICANT: Vijn, Irma M.C.
APPLICANT: Vijn, Irma M.C.
APPLICANT: Sijmons, Peter C.
TITLE OF INVENTION: A SITUCTURE for presenting desired peptide sequences
FILE RPFBRENCE: 2183-5610US
CURRENT APPLICATION NUMBER: US/10/316,194
CURRENT APPLICATION NUMBER: US 10/016,516
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Petentin Ver: 2.1
SEQ ID NO 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid OTHER INFORMATION: sequence of iMab600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: VAP amino acid OTHER INFORMATION: sequence of iMab1100
Gaps
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Indels
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  3,
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; Pred. No. 6.7e-
0; Mismatches
0; Mismatches
                                            23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ORVEILEGRIECVLSNLRGRIRY 23
                                                                                                                                                                                      Sequence 35, Application US/10316194 Publication No. US20030215914A1 GENERAL INFORMATION:
                                       1 ORVEILEGRIECVLSNLRGRIRY
                                                                                  46 ORVEILNMGTECVLSNLRGRTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 87.0%;
Matches 20; Conservative
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20; Conservative
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; LOCATION: (1)..(109)
US-10-316-194-43
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; LOCATION: (1)..(109)
US-10-316-194-35
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  Matches
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Search completed: May 6, 2004, 12:48:22 Job time : 43 secs
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| Sequence 11. Application US/09947063
| Publication No. US20030059775A1
| GENERAL INFORMATION:
| APPLICANT: Padigaru et al. |
| TITLE OF INVENTION: No. US20030059775A1e1 Proteins and Nucleic Acids Encoding Same PILE REFERENCE: 21402-112
| CURRENT FILING DATE: 2001-09-05 |
| PRIOR APPLICATION NUMBER: 60/229,980 |
| PRIOR APPLICATION NUMBER: 60/229,980 |
| PRIOR PILING DATE: 2000-09-05 |
| PRIOR FILING DATE: 2000-09-05 |
| NUMBER OF SEQ ID NOS: 30 |
| SEQ ID NO 11 |
| LENGTH: 1026
                                                                                                                                                                                          Sequence 4, Application US/09947063
Publication No. US20030059775A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030059775A1e1 Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-112
CURRENT PILION NUMBER: US/09/947,063
CURRENT FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 60/229,990
PRIOR FILING DATE: 2000-09-05
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                    4; Indels
Similarity 82.6%; Pred. No. 8.6e-06; 9; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                              46 ORVEILNMGTESVLSNLRGRTRY 68
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US-09-728-912-7
; Sequence 7, Application US/09728912
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illarity 71.4%;
Conservative
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CORGANISM: Homo sapiens
US-09-947-063-11
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 10; Conserva
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Gaps
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APPLICANT: Holloway, James L.
TITLE OF INVENTION: Tumor Necrosis Factor-Stimulated Gene
TITLE OF INVENTION: and Protein
FILE REFERENCE: 99-940S
CURRENT APPLICATION NUMBER: US/09/728,912
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/169,252
NUMBER OF PS 1999-12-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                  DB 9; Length 49
                                                                                                                                                                                                                                                                                                                                                                                  Score 49; DB 9
Pred. No. 2.4;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0%;
Matches 10; Conservative 4
                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-09-728-912-7
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